

2 32
CTT TCA GAA GCC CGG GAG AGC GTC TTG GGG GAT TTG CTG AAG GTT GTG CTG TAC AGC CTG
leu ser glu ala arg glu ser val leu gly asp leu leu lys val val leu tyr ser leu

62 92
GGC AGT GCC CAG AGT GCC CTC TTC TTG CAG CAT GGC CTG GCC ACC CAG AGG GCC CTT GTG
gly ser ala gln ser ala leu phe leu gln his gly leu ala thr gln arg ala leu val

122 152
TCC AAG TTC CCG GAG CTG CTG TTC GAG GAG GAC ACG GAG CTG TGT GCC GAC CTG TGC CTG
ser lys phe pro glu leu leu phe glu glu asp thr glu leu cys ala asp leu cys leu

182 212
AGG CTC CTA CGA CAC TGT GGC AGC CGC ATC AGC ACC ATC CGC ACG CAC GCC AGC GCC TCG
arg leu leu arg his cys gly ser arg ile ser thr ile arg thr his ala ser ala ser

242 272
CTG TAC CTG CTC ATG CGA CAG AAC TTC GAG ATC GGC CAC AAC TTT GCC CGT GTG AAG ATG
leu tyr leu leu met arg gln asn phe glu ile gly his asn phe ala arg val lys met

302 332
CAG GTC ACC ATG TCT CTC TCG TCC CTG GTG GGG ACG ACG CAG AAC TTC AGT GAA GAG CAC
gln val thr met ser leu ser ser leu val gly thr thr gln asn phe ser glu glu his

362 392
CTG CGA CGT TCA CTC AAA ACC ATC CTC ACC TAT GCT GAG GAG GAC ATG GGG CTG CGG GAC
leu arg arg ser leu lys thr ile leu thr tyr ala glu glu asp met gly leu arg asp

422 452
AGC ACC TTC GCA GAG CAG GTC CAG GAC CTG ATG TTC AAC CTG CAC ATG ATC CTG ACG GAC
ser thr phe ala glu gln val gln asp leu met phe asn leu his met ile leu thr asp

482 512
ACG GTG AAG ATG AAG GAA CAC CAG GAG GAC CCT GAG ATG CTC ATC GAC CTC ATG TAC AGA
thr val lys met lys glu his gln glu asp pro glu met leu ile asp leu met tyr arg

542 572
ATT GCC CGG GGC TAC CAG GGC TCA CCG GAC CTT CGG CTG ACC TGG TTG CAG AAC ATG GCC
ile ala arg gly tyr gln gly ser pro asp leu arg leu thr trp leu gln asn met ala

602
GGG AAG CAC GCG GAG CTG GGC AAC CAC GCC GAG GCC GCC CAG TGC ATG GTG CAC GCG GCC
gly lys his ala glu leu gly asn his ala glu ala ala gln cys met val his ala ala

xxxxxxxxxxxxxxxxx transmembrane domain xxxxxxxxxxxxxx

XXXXXXXXXXXXXXXXXXXXXXXXXXXXX	692
GCC CTC GTG GCT GAG TAC CTC GCC CTG CTC GAG GAC CAC CGC CAC CTG CCC GTG GGC TGC	
ala leu val ala glu tyr leu ala leu leu glu asp his arg his leu pro val gly cys	
722	752
GTT TCC TTC CAG AAC ATC TCA TCC AAT GTG CTA GAG GAG TCC GCC ATC TCC GAC GAC ATC	
val ser phe gln asn ile ser ser asn val leu glu glu ser ala ile ser asp asp ile	
782	812
CTG TCG CCC GAC GAG GAG GGC TTC TGC TCC GGG AAG CAC TTC ACT GAG CTG GGG CTG GTA	
leu ser pro asp glu glu gly phe cys ser gly lys his phe thr glu leu gly leu val	
842	872
GGG TTG CTG GAA CAG GCA GCC GGC TAC TTC ACC ATG GGC GGG CTC TAC GAG GCG GTG AAT	
gly leu leu glu gln ala ala gly tyr phe thr met gly gly leu tyr glu ala val asn	
902	932
GAG GTC TAC AAG AAC CTC ATC CCC ATC CTG GAA GCC CAC CGT GAC TAC AAG AAG CTG GCC	
glu val tyr lys asn leu ile pro ile leu glu ala his arg asp tyr lys lys leu ala	
962	992
GCG GTG CAC GGC AAA CTG CAG GAG GCC TTC ACC AAG ATC ATG CAC CAG AGT TCC GGC TGG	
ala val his gly lys leu gln glu ala phe thr lys ile met his gln ser ser gly trp	
1022	xxxxx ITAM xxxxx 1052
GAG CGC GTG TTC GGG ACG TAT TTC CGC GTG GGC TTC TAC GGC GCC CAC TTC GGT GAC CTG	
glu arg val phe gly thr tyr phe arg val gly phe tyr gly ala his phe gly asp leu	
1082	1112
GAT GAG CAG GAG TTT GTG TAC AAG GAG CCA TCG ATC ACG AAG CTG GCA GAG ATC TCA CAC	
asp glu gln glu phe val tyr lys glu pro ser ile thr lys leu ala glu ile ser his	
1142	1172
CGG CTG GAG GAG TTC TAC ACG GAG AGA TTT GGC GAC GAC GTC GTT GAG ATT ATC AAA GAC	
arg leu glu glu phe tyr thr glu arg phe gly asp asp val val glu ile ile lys asp	
1202	1232
TCT TAC CCT GTG GAC AAG TCC AAG CTT GAC TCA CAA AAG GCC TAC ATC CAG ATC ACG TAT	
ser tyr pro val asp lys ser lys leu asp ser gln lys ala tyr ile gln ile thr tyr	
1262	1292
GTG GAA CCG TAC TTT GAT ACC TAC GAG CTC AAG GAC CGG GTG ACC TAC TTT GAC CGC AAC	
val glu pro tyr phe asp thr tyr glu leu lys asp arg val thr tyr phe asp arg asn	
1322	1352
TAT GGG CTT CGC ACA TTC CTG TTC TGC ACG CCG TTC ACG CCG GAT GGG CGC GCA CAC GGG	
tyr gly leu arg thr phe leu phe cys thr pro phe thr pro asp gly arg ala his gly	

1382 1412
GAG CTG CCC GAG CAA CAC AAG CGT AAG ACG CTG CTC AGC ACC GAC CAC GCC TTC CCC TAC
glu leu pro glu gln his lys arg lys thr leu leu ser thr asp his ala phe pro tyr

1442 1472 |xxxxxxxxxxx
ATC AAG ACT CGC ATC CGT GTG TGC CAC CGG GAG GAG ACG GTG CTG ACG CCA GTG GAG GTG
ile lys thr arg ile arg val cys his arg glu glu thr val leu thr pro val glu val

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coile coil 1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
GCC ATC GAG GAC ATG CAG AAG AAG ACA CGG GAG CTG GCC TTT GCC ACC GAG CAG GAC CCA
ala ile glu asp met gln lys lys thr arg glu leu ala phe ala thr glu gln asp pro

xx |
CCA GAT GCT AAG ATG CTA CAG ATG GTG CTT CAG GGC TCT GTA GGG CCC ACC GTG AAC CAG
pro asp ala lys met leu gln met val leu gln gly ser val gly pro thr val asn gln

1622 1652
GGT CCC CTG GAG GTG GCC CAG GTG TTT TTA GCA GAG ATC CCG GAA GAC CCC AAG CTC TTC
gly pro leu glu val ala gln val phe leu ala glu ile pro glu asp pro lys leu phe

1682 1712
CGG CAT CAC AAC AAA TTG CGG CTC TGC TTC AAG GAC TTC TGC AAG AAA TGT GAG GAT GCG
arg his his asn lys leu arg leu cys phe lys asp phe cys lys lys cys glu asp ala

xx Coiled coil 2 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
CTG CGG AAA AAT AAG GCC CTG ATT GGG CCG GAC CAG AAG GAG TAC CAC CGT GAG CTG GAG
leu arg lys asn lys ala leu ile gly pro asp gln lys glu tyr his arg glu leu glu

xx |
CGC AAC TAC TGC CGC CTG CGG GAG GCT CTG CAG CCC CTG CTT ACC CAG CGC CTG CCC CAG
arg asn tyr cys arg leu arg glu ala leu gln pro leu leu thr gln arg leu pro gln

1862 1892
CTG ATG GCA CCC ACC CCA CCC GGC CTC AGG AAC TCC TTG AAC AGA GCA AGT TTC CGA AAG
leu met ala pro thr pro pro gly leu arg asn ser leu asn arg ala ser phe arg lys

1922 1952
GCA GAC CTC TGA GCC CAC AAG GAC CAA AGC TGT ACC TAG AGG AAC CAG CAC CCG GGC CTC
ala asp leu STP

1982 2012
AGC TGT CTG TGC TGC GAG GGG AGT CTG CCC TGG TGC CCA CTG GGC TGT GGG GTG ACC ACA

2042 2072
CTG TAC TTG GGG CTG GGC CCT CTG CCC CTG TGT CCC CAT CTG TGT GCA CTG ATG CTT CCT

2102 2132
CCC TTT TTT AAT TTA AAA TGG TTT TTA TAA GCA AAA AAA AAA AAA AAA

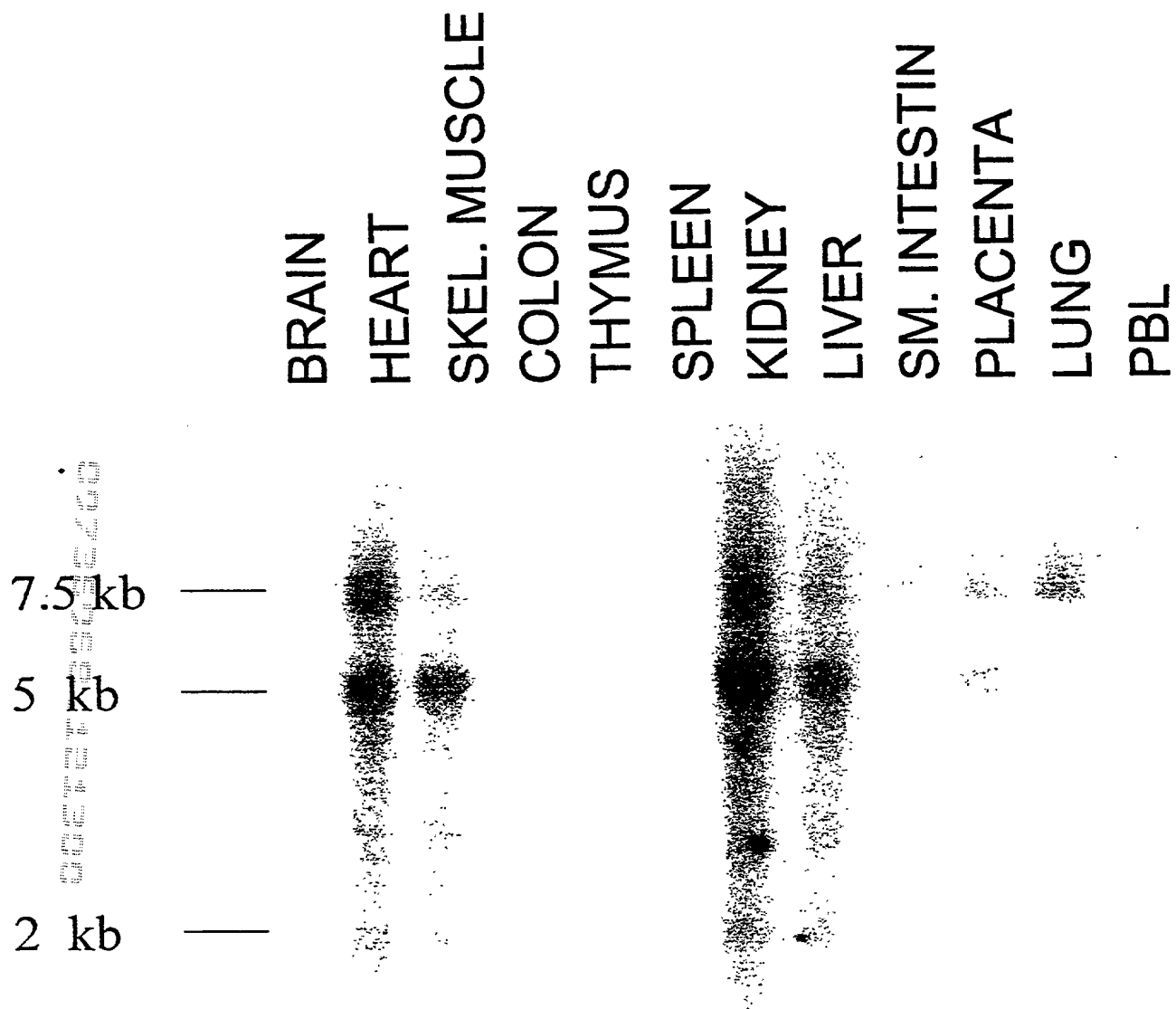


FIG. 2

HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----VLHHHQNPFEFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTSAFAAVLHHHQNPFEFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	PVSANLPSGYLGQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat	PVSANLPSGYLGQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSISLISNSARV
HC5	-----

HC2A	-----
KIAA	OKTESGAQALGNELVKYLSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	OKTESGAQALGNELVKYLSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
HC4	-----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5	-----

HC2A I I H V V A Q C H G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E L T K S M T T I L K P S A D F L T S N
 KIAA I I H V V A Q C H E E G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E L T K S M T T I L K P S A D F L T S N
 rat -----
 HC4 L F H I V S K C H E E G L D S Y L S S F I K Y S F R P G K P S A P Q A P L I H E T L A T M M I A L L K Q S A D F L A I N
 HC1 L P D I V A K C H E E Q L D H S V Q S Y I K F V F K T R --- A C K E R P V H E D L A K N V T G L L K - S N D S P T V K
 HC3 T Q A M D R S C N R M S S H T E T S S F L Q T L T G R L P ---- T K K L F H E E L A L Q W V V C S G -- S V R --- E
 HC5 -----

Cadherin
 Cleavage

HC2A K L L R Y S W F F F D V L I K S M A Q H L I E N S K V K L I R N Q R F P A S Y H H A A E T V V N M L M P H I T Q K F G D
 KIAA K L L K Y S W F F F D V L I K S M A Q H L I E N S K V K L I R N Q R F P A S Y H H A V E T V V N M L M P H I T Q K F R D
 rat -----
 HC4 K L L K Y S W F F F E I I A K S M A T Y L L E E N K I K L T H G Q R F P K A Y H H A L H S L F L A I T - I V E S Q Y A E
 HC1 H V L K H S W F F F A I I L K S M A Q H L I D T N K I Q L E R P Q R F P E S Y Q N E L D N L V M V L S D H V I W K Y K D
 HC3 S A L Q Q A W F F F E L M V K S M V H H L Y F N D K L E A E R K S R F P E R F M D D I A A L V S T I A S D I V S R F Q K
 HC5 -----

HC2A N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S -- C F A P G D P K T L F E Y K F E F L
 KIAA N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S -- C F A P G D P K T L F E Y K F E F L
 rat -----
 HC4 I P K E S R N V N Y S L A S F L K C C L T I M D R G F V F N L I N --- D Y I S -- G F S P K D P K V L A E Y K F E F L
 HC1 A L E E T R R A T H S V A R F L K R C F T F M D R G C V F K M V N --- N Y I S -- M F S S G D L K T L C Q Y K F D F L
 HC3 D T E M V E R L N T S L A F F L N D L L S V M D R G F V F S L I K S C Y K Q V S S K L Y S L P N P S V L V S L R L D F L
 HC5 -----

HC2A R V V C N H E H Y I P L N L P M ---- P F G K G R I Q R ----- Y Q D L Q L ---- D Y S L T D E F
 KIAA R V V C N H E H Y I P L N L P M ---- P F G K G R I Q R ----- Y Q D L Q L ---- D Y S L T D E F
 rat -----
 HC4 Q T I C N H E H Y I P L N L P M ---- A F A K P K L Q R ----- V Q D S N L ---- E Y S L S D E Y
 HC1 Q E V C Q H E H F I P L C L P I R S A N I P D P L T P S E S ----- T Q E L H A S D M P E Y S V T N E F
 HC3 R I I C S H E H Y V T L N L P C S L T P P A S P S V S S A T S Q S S G F S T N V Q D Q K I A N M F E L S -- V P F
 HC5 ----- M N A D T A P T S P C P S I S --- S Q N S S S C S S F Q D Q K I A S M F D R T S R V P A

Cadherin
 EC motif

HC2A C R N H F L V G I L L R E V G T A L Q E F R E --- V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
 KIAA C R N H F L V G I L L R E V G T A L Q E F R E --- V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
 rat -----
 HC4 C K H H F L V G I L L R E T S I A L Q D N Y E --- I R Y T A I S V I K N L L I K H A F D T R Y Q H K N Q Q A K I A Q
 HC1 C R K H F L I G I L L R E V G F A L Q E D Q D --- V R H L A L A V L K N L M A K H S F D D R Y R E P R K Q A Q I A S
 HC3 R Q Q H Y L A G I V L T E L A V I L D P D A E G L F G L H K K V I N M V H N L L S S H D S D P R Y S D P Q I K A R V A M
 HC5 S S T S - S P G I L F T E L A A A L D A E G E G I S E V Q R K A V S A I H S L L S S H D L D P R C V K P E V K V K I A A

HC2A L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
 KIAA L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
 rat -----
 HC4 L Y L P F V G L L L E N I Q R L A G R D T L Y S C A M P N S A S R D E F P C G ---- F T S P -- A N -- R G S L S
 HC1 L Y M P L Y G M L L D N M P R I Y L K D L Y P F T V N T S N Q G S R D D L S T N G G F Q S Q T A I K H A N S V D T S F S
 HC3 L Y L P L I G I I M E T V P Q L Y D F T E T H N Q R G R P I C I A T D D Y E S E ----- S G --- S M I S
 HC5 L Y L P L V G I I L D A L P Q L C D F T V A D T R R Y R --- T S G S D E E Q E ----- G A --- G A I T

HC2A KDLGAISSG PYTTSTPNINSVRNADSRGSLISTDSGNS RNSEKSNSLDKHQSS
 KIAA KDLGAISSG PYTTSTPNINSVRNADSRGSLISTDSGNS RNSEKSNSLDKHQSS
 rat -----
 HC4 TDKDTAYGSFQNG-----HGIKREDSRGS LIP-EGATGFPDQGN TGEN-----TRQS
 HC1 KDV LNSIAAFSS-----IAISTVNHADSRASLASLD SNPSTNEKSSEKTDNCEKIPRPL
 HC3 QTVAMAIAGTSVPO-----LTRPGSFLLTSTSGRQHT-----
 HC5 QNVALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----

HC2A TLGNSVVRCDKLDQSEIKSLLMCFLYILKSM SDDALFTYWN-KASTSELMDFFTI SEVCL
 KIAA TLGNSVVRCDKLDQSEIKSLLMCFLYILKSM SDDALFTYWN-KASTSELMDFFTI SEVCL
 rat -----
 HC4 STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDTLLTYWN-KVSPQELINILILLEVCL
 HC1 ALIGSTLRFDRLDQAETRSLLMCF LHMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL
 HC3 -----TFSAESSRSL LICLLWVLKN-ADETVLQKWFTDLSVLQ LNRLLDLLYLCV
 HC5 -----MLNADTTNRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV

HC2A HQFOYMGKRYIARNQEG LG--PIVHDRKS-----QTLPVSRNRTGMM
 KIAA HQFOYMGKRYIAR-----TGMM
 rat -----
 HC4 FHFRYMGKRNIARVHDAWLSKHFGIDRKS-----QTMPALNRNSGVM
 HC1 QNFRYLGRNIIRKIAAAF--KFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHK
 HC3 SCFEYKGGKVFERMNSLT FK--KSKDMRAK-----LEEAILGSIGARQEMV
 HC5 LCFEYKGGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGE GARGEMM

HC2A HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
 KIAA HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
 rat -----
 HC4 QARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVS
 HC1 QHRSQTLPIIRGK--NALS NPKL----LQMLDNTMTSNSNEIDIVHHVDTEAN IATEGC
 HC3 RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNT EKLDKSRAEIEHEALIDGNLATEAN
 HC5 RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH

HC2A LTALD TLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSE TALKNVFTALRS LIY
 KIAA LTALD TLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSE TALKNVFTALRS LIY
 rat -----KLSRGHSP LMKKVFDVYLCFLQKHQSE MALKNVFTALRS LIY
 HC4 LTVLDTISFFTQC FKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
 HC1 LTILDVLSLFTQTHQRQLQCCDCQNSLMKRGFDTYMLFFQV NQSATALKHVFASLRLEVC
 HC3 LIILD TLEIVVQTVS--VTES--KESILGGVLK VLLHSMACNQSAVYLQHC FATQRALVS
 HC5 LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNC DQSTTYLTHCFATLRALIA

HC2A KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYT GKKS FVRTH
 KIAA KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYT GKKS FVRTH
 rat KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYT GKKS FVRTH
 HC4 KFPSAFFKGRVNMCAAF CYEVLKCCTSKISS TRNEASALLYLLMRNNFEYTKRKTFLRTH
 HC1 KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYL FMRKNFEFNKQKSIVRSH
 HC3 KFPELLFEEETEQCADLCLRLLRHCSSSIGTIRSHPSASLYLLMRQNF EIGN--NFA RVK
 HC5 KFGDLLFEEVEQC FDLCHQVLHHCSSSMDVTRSQACATLYLLMRFSFGATS--NFA RVK

HC2A LQV IISVSQLIADVVGIGETRFQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLM
 KIAA LQV IISVSQLIADVVGIGETRFQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLM
 rat LQV IISLSQLIADVVGIGETRFQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLM
 HC4 LQIIIAVSQLIADVALSGGSRFQESLFI INNFANS DRPMLARAFPAEVKDLTKRIRTVLM
 HC1 LQLIKAVSQLIAD-AGIGGSRFQHS LAITNNFANGDKQMKNSNFP AEVKDLTKRIRTVLM
 HC3 MQVPMSLSSLVGTSQNFNEEFLRRSLKTI LTYAEEDLELRETTFPDQVQDLVFNLMHILS
 HC5 MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMTFPPTQVEELL CNLNSILY

FIG. 3
 3 of 5

		Transmembrane
HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGL	LSEAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGL	LSEAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGL	LSEAAMCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKRWLDSMAIHVKNGL	FSEAAMCYVHV
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAIHARNG	LSEAAMCYIHI
HC3	DTVKMKEHQEDPEMLIDLMYRIAKGYQTSPLRLTLWLQNMAGKHSERS	HAEAAQCLVHS
HC5	DTVKMREFQEDPEMLMDLMYRIAKSYQASPLRLTLWLQNMAEKHTKKK	GYTEAAMCLVHA

	domain	SH3	
HC2A	TALVAEYILTRKGV-----		FRQGCTAFRUITPN
KIAA	TALVAEYILTRKEA-----	VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRUITPN	
rat	TALVAEYILTRKEAD-----	LALQREPPVPFYSHTSCQKSRGGMFRQGCTAFRUITPN	
HC4	AALVAEFLHRKKL-----		FPNGCSAFKKITPN
HC1	AALIAEYILKRKGWYKVEKIC	TASLLSEDPHPCDSNSLLTTPSGGSMFMSGWPAFLSITPN	
HC3	AALVAEYILSMLED-----		RKYLPGVCVTFQNISSN
HC5	AALVAEYILSMLED-----		HSYLPVGSVSFQNISSN

		ITAM
HC2A	IDEEASMMEDVGMQD-----	VHFNEVDVLMELLEQCADGLWKAERYELIADIYKLIIP
KIAA	IDEEASMMEDVGMQD-----	VHFNEVDVLMELLEQCADGLWKAERYELIADIYKLIIP
rat	IDEEASMMEDVGMQD-----	VHFNEVDVLMELLEQCADGLWKAERLRAGLLTSINSSSP
HC4	IDEEGAMKEDAGMMD-----	VHYSEEVLLLELLEQCVNGLWKAERYETIISEISKLI GPI
HC1	IKKEGAAKEDSGMHD-----	TPYNENILVEQLYMCGEFLWKSEYELIADVNPPIIAV
HC3	VLEESAVSDDVVPDEEGICSGKYFTESGLVGLLEQAAASFMSAGMYEAVNEVYKVLIP	
HC5	VLEESVSVSEDTLSPDEGDVCGAQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKVLIP	

	ITAM	ITAM	ITAM	ITAM
HC2A	YEKRRD-----			
KIAA	YEKRRDFERLAHLVDTHIRRAYSKVTEVMHSGRRLGTYFRVAFFGQAQYQFTDSETDVE			
rat	SMKSGGTLETHLYDTIHRHYSKVTEVITR-----	A	AGSWDLLPGGLFGQ	
HC4	YENRREFENLTQVVRTIHGAYTKILEVMHTKKRLLG-----		TFFRVAFYGO	
HC1	FEQRDFKKLSDLVDYDHRSYLKVAEVVNSEKRLFG-----		RYFRVAFYGO	
HC3	HEANRDAKKLSTIHGKLQEAFSKIVHQSTGWERMFG-----		TYFRVGFYGO	
HC5	LEAHREFRKLTLTHSKLQRAFDIVNKH--KRMFG-----		TYFRVGFFG-	

	ITAM	ITAM
HC2A	-FFEDEDGKEYIYKEPKLTPLSEISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA	
KIAA	GFFEDEDGKEYIYKEPKLTPLSEISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA	
rat	GFFEDEDGKEYIYKEPKLTPLSEISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA	
HC4	SFFEEDGKEYIYKEPKLTGLSEISLRLVKLYGEKFGTENVKIIQDSKVNPAKELDPKYA	
HC1	GFFEEEGKEYIYKEPKLTGLSEISQRLKLYADKFGADNVKIIQDSNVNPKDLDPKYA	
HC3	TKFGDLDEQEFVYKEPAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKA	
HC5	SKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGOFGAEFVEVIKdstpvdktklDPNKA	

	ITAM
HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA
rat	YIQVTHVTPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA
HC4	HIQVTVKPYFDDKELTERKTEFERNHNIISRFVFEAPYTLGSKKQGCIEEQCKRRTILTT
HC1	YIQVTVVTPFFEEKEIEDRKTD FEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILTT
HC3	YIQITYVEPYFDTYEMKDRITYFDKNYNLRREMYCTPFTLDGRAHGEHQFKRKTILTT
HC5	YIQITTFVEPYFDEYEMKDRVITYFEKNFNLRREMYTTPFTLEGRPRGELHEQYRRNTVLT

Coiled-Coil 1

HC2A	IHCFFPYVKKRIPVMYQHHTDLNFI	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
KIAA	IHCFFPYVKKRIPVMYQHHTDLNFI	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
rat	IHCFFPYVKKRIPVMYQHHTDLNFI	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
HC4	SNSFFPYVKKRIPINCEQQINLKH	IDGATDEIKDKTAELOKLCSSSTDVMIQLQLKLQGSV
HC1	SHLFFPYVKKRIQVISQSSTELNFI	IEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLQGSV
HC3	SHAFPIYIKTRVNVTHKEEIIILTF	IEVAIEDMOKKTQELAFATHQDPADPKMLQMVLOGSV
HC5	MHAFPIYIKTRISVIQKEEFVLTF	IEVAIEDMOKKTQELAFATHQDPADPKMLQMVLOGSV

Coiled-Coil 2

HC2A	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQAL	LAVNERLIKEDQLE
KIAA	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQAL	LAVNERLIKEDQLE
rat	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQAL	LAVNERLIKEDQLE
HC4	SVQVNAGPLAYARAFLLDSQASKYPPKKVSELKDMFRKFIQACSI	LELNERLIKEDQVE
HC1	SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQAL	LDVNERLIKEDQLE
HC3	GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDAL	RKNKSLIGPVQKE
HC5	GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEA	VEKNKRLITADQRE

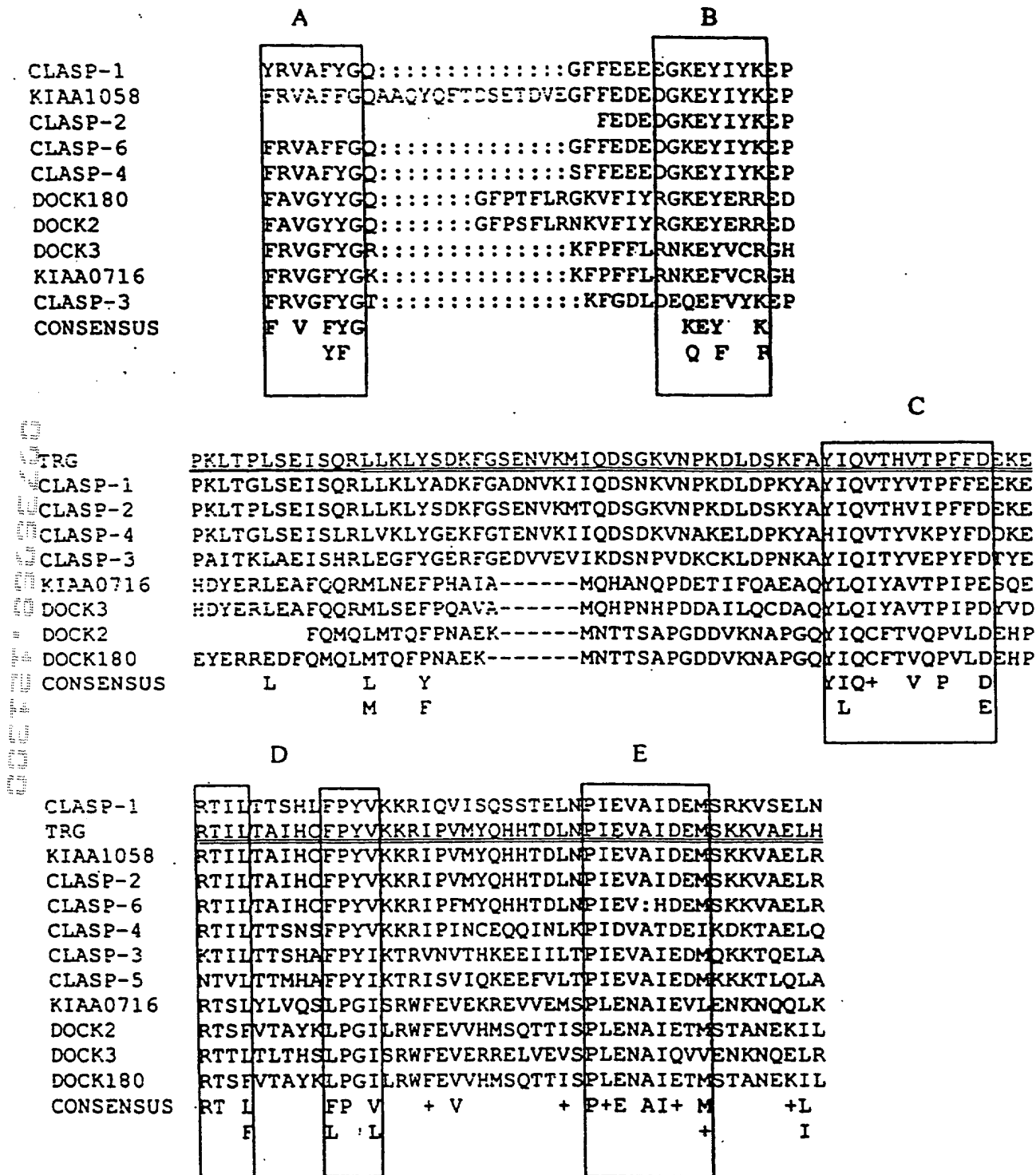
Coiled-Coil 2

HC2A	YQEEMKANYREMAKELSEIMHE	QICPLEEKTS-VLPNSLHIFNAISGTPSTMVHGMTSS
KIAA	YQEEMKANYREMAKELSEIMHE	QLG-----
rat	YQEEMKANYREIRKELSDIIVER	ICPGEDKRATKFPAPHLQRHQRDTNKHSGSRVDQFELS
HC4	YHEGLKSNFRDMVKELSDIIEH	QILQEDTMHSPWMSNTLHVFCASISGTSDDRGYGSPPRYA
HC1	YQEELRSHYKMDLSELSTVMNE	QITGRDDLK---RGVDQCTCTRVISKATPALPTVSISS
HC3	YQRELG-----KLSS-----	PZ-----
HC5	YQQELKKNYNKLKENLRPMIEP	KIPELYKPIFRVESQKRDSFHRSSFRCETQLSQGSZ-

PRM

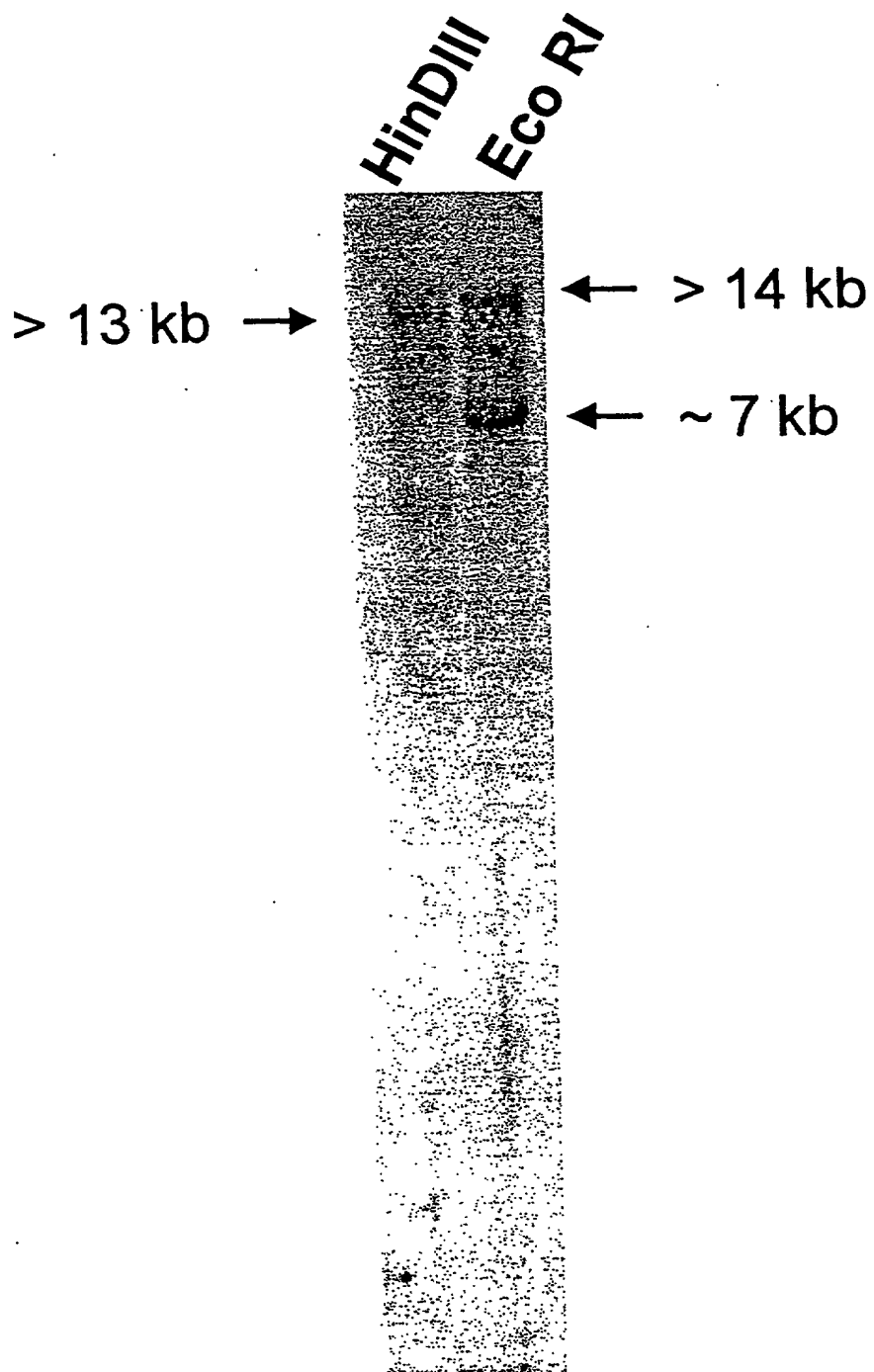
HC2A	SSVVZ-----
KIAA	-----
rat	CVTLPHPEPHVGTFCFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWTVIFNSRFYRSWGK
HC4	EVZ-----
HC1	SAEVZ-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	-----
rat	VHIFF
HC4	-----
HC1	-----
HC3	-----
HC5	-----



	F	G	
CLASP-1	SLQLKLQGSVSVKVNAGPMA	YARAFLEETNAKKYP	DNQV--KILKEIFRQFADACGQALD
TRG	KLQLKLQGSVSVQVNAGPLA	YARAFLLDDTNTKRY	DNKV--KILKEVFRQFVEACGQALA
KIAA1058	KLQLKLQGSVSVQVNAGPLA	YARAFLLDDTNTKRY	DNKV--KILKEVFRQFVEACGQALA
CLASP-2	KLQLKLQGSVSVQVNAGPLA	YARAFLLDDTNTKRY	DNKV--KILKEVFRQFVEACGQALA
CLASP-6	KLQLKLQGSVSVQVNAGPLA	YARAFLLDDTNTKRY	DNKV--KILKEVFRQFVEACGQALA
CLASP-3	MLQMLQGSVGTTVNQGLE	VAQVFLSE--IPSDP	KLFRHHNKLRLCFKDFTKRCEDALR
CLASP-4	QLQLKLQGCVSQVNAGPLA	YARAFLLDSQASKYP	PKKVSELKDMFRKFI--QACSI
CLASP-5	MLQMLQGSVGTATVNQGLE	VAQVFLAE--IPADP	KLFRHHNKLRLCFKEFIMRCGEAVE
KIAA0716	PLTMCLNGVIDAAVNGGVS	RYQEAFVKEYILSHPE	DGEKIARLRRLMLEQAQILEFGLA
DOCK2	PLSMLLNGIVDPAVMGGE	FAKYEKAFTEEYVRDH	PEQDKLTHLKDIAWQIPFLGAGIK
DOCK3	ILSMCLNGVIDAAVNGGI	ARYQEAFDDKDYINKH	PGDAEKITQLKELMQEQVHVLGVGLA
DOCK180	PLSMLLNGIVDPAVMGGE	FAKYEKAFTEEYVRDH	PEAHEKIEKLKDIAWQIPFLAEGIR
CONSENSUS	L M L+G V VN G	Y AFL + + P	L+
	L I	V V F +	I

DOCK2=KIAA0289
 DOCK3=KIAA0299
 CLASPvariant=KIAA1058



genomic DNA

FIG. 4

-12 -1
GACGCGAGGACC

1/1	31/11
ATG GCT GCC TCC GAG CGC CGC GCC TTC GCG CAC AAG ATC AAC AGG ACG GTG GCC GCA GAG	
Met ala ala ser glu arg arg ala phe ala	his lys ile asn arg thr val ala ala glu
61/21	91/31
GTG CGG AAG CAG GTG TCC CGG GAA CGC AGT GGC TCC CCC CAC TCC AGC AGG CGC TGC AGC	
val arg lys gln val ser arg glu arg ser	gly ser pro his ser ser arg arg cys ser
121/41	151/51
AGC TCC CTG GGG GTC CCA CTG ACT GAA GTT GTC GAG CCC CTG GAC TTT GAG GAT GTA CTT	
ser ser leu gly val pro leu thr glu val	val glu pro leu asp phe glu asp val leu
181/61	211/71
CTG AGC CGG CCA CCA GAT GCT GAG CCC GGG CCC CTC AGG GAC CTG GTA GAA TTC CCA GCT	
leu ser arg pro pro asp ala glu pro gly	pro leu arg asp leu val glu phe pro ala
241/81	271/91
GAT GAC TTG GAG CTG CTG CTG CAG CCC CGG GAA TGC CGG ACC ACG GAG CCC GGG ATC CCC	
asp asp leu glu leu leu leu gln pro arg	glu cys arg thr thr glu pro gly ile pro
301/101	331/111
AAG GAT GAA AAA CTG GAT GCC CAG GTG AGG GCC GCG GTG GAG ATG TAT ATT GAG GAC TGG	
lys asp glu lys leu asp ala gln val arg	ala ala val glu met tyr ile glu asp trp
361/121	391/131
GTC ATT GTC CAC AGA AGG TAT CAG TAC CTG AGT GCA GCA TAC AGC CCC GTC ACC ACA GAC	
val ile val his arg arg tyr gln tyr leu	ser ala ala tyr ser pro val thr thr asp
421/141	451/151
ACA CAG CGG GAG CGA CAG AAG GGC CTC CCC CGC CAG GTC TTT GAG CAG GAT GCT TCT GGA	
thr gln arg glu arg gln lys gly leu pro	arg gln val phe glu gln asp ala ser gly
481/161	511/171
GAC GAG AGG TCC GGC CCT GAG GAC TCG AAT GAC TCC CGG CGT GGC TCG GGC TCC CCG GAA	
asp glu arg ser gly pro glu asp ser asn	asp ser arg arg gly ser gly ser pro glu
541/181	571/191
GAC ACC CCT CGA AGC AGT GGT GCC TCT AGC ATC TTC GAC CTG AGG AAC CTG GCA GCT GAC	
asp thr pro arg ser ser gly ala ser ser	ile phe asp leu arg asn leu ala ala asp
601/201	631/211
TCA TTG CTG CCC TCT CTG CTA GAG CGG GCG GCC CCA GAA GAT GTG GAC CGG CGC AAT GAA	
ser leu leu pro ser leu leu glu arg ala	ala pro glu asp val asp arg arg asn glu
661/221	691/231
ACC CTT CGA CGG CAG CAC CGG CCC CCG GCC CTG CTC ACC CTC TAC CCG GCA CCT GAC GAG	
thr leu arg arg gln his arg pro pro ala	leu leu thr leu tyr pro ala pro asp glu
721/241	751/251
GAT GAA GCC GTG GAA CGC TGT AGC CGC CCA GAG CCA CCC CGC GAG CAC TTT GGA CAA AGG	
asp glu ala val glu arg cys ser arg pro	glu pro pro arg glu his phe gly gln arg
781/261	811/271
ATC TTG GTC AAG TGT CTG TCG CTC AAG TTC GAG ATT GAA ATT GAG CCC ATC TTT GGG ATC	
ile leu val lys cys leu ser leu lys phe	glu ile glu pro ile phe gly ile
841/281	871/291
TTG GCT CTG TAT GAT GTG CGG GAG AAA AAG AAG ATC TCG GAG AAC TTC TAC TTC GAC CTG	
leu ala leu tyr asp val arg glu lys lys	lys ile ser glu asn phe tyr phe asp leu
901/301	931/311
AAC TCG GAC TCC ATG AAG GGG CTG CTT CGG GCT CAT GGC ACC CAC CCT GCC ATC TCC ACC	
asn ser asp ser met lys gly leu leu arg	ala his gly thr his pro ala ile ser thr
961/321	991/331
CTG GCC CGC TCT GCC ATC TTC TCT GTG ACC TAC CCC TCA CCT GAC ATC TTC CTG GTC ATC	
leu ala arg ser ala ile phe ser val thr	tyr pro ser pro asp ile phe leu val ile
1021/341	1051/351
AAG TTG GAG AAG GTG CTT CAG CAA GGG GAC ATC AGT GAG TGC TGT GAG CCT TAC ATG GTG	
lys leu glu lys val leu gln gln gly asp	ile ser glu cys cys glu pro tyr met val
1081/361	1111/371

TTG AAA GAA GTG GAC ACA GCC AAG AAC AAA GAG AAG CTA GAG AAG CTG CGC CTG GCG GCC
 leu lys glu val asp thr ala lys asn lys glu lys leu glu lys leu arg leu ala ala
 1141/381 1171/391
 GAG CAG TTC TGC ACC CGC CTG GGC CGC TAC CGC ATG CCC TTC GCC TGG ACG GCC GTG CAC
 glu gln phe cys thr arg leu gly arg tyr arg met pro phe ala trp thr ala val his
 1201/401 1231/411
 TTG GCC AAC ATC GTG AGC AGC GCT GGG CAG CTG GAC CGG GAC TCT GAC TCG GAG GGC GAG
 leu ala asn ile val ser ser ala gly gln leu asp arg asp ser asp ser glu gly glu
 1261/421 1291/431
 CGC CGG CCA GCC TGG ACA GAC CGC CGC CGT CGG GGG CCC CAG GAC CGG GCG AGT AGT GGG
 arg arg pro ala trp thr asp arg arg arg arg gly pro gln asp arg ala ser ser gly
 1321/441 1351/451
 GAC GAC GCC TGC AGC TTC TCT GGC TTC CGT CCA GCC ACG CTA ACT GTC ACA AAC TTC TTT
 asp asp ala cys ser phe ser gly phe arg pro ala thr leu thr val thr asn phe phe
 1381/461 1411/471
 AAG CAG GAG GCT GAG CGA CTC AGT GAC GAG GAC CTC TTC AAG TTC CTG GCT GAC ATG AGG
 lys gln glu ala glu arg leu ser asp glu asp leu phe lys phe leu ala asp met arg
 1441/481 1471/491
 CGC CCG TCG TCC CTG CTG CGG CGA CTA CGT CCT GTG ACT GCC CAG CTC AAG ATC GAC ATT
 arg pro ser ser leu leu arg arg leu arg pro val thr ala gln leu lys ile asp ile
 1501/501 1531/511
 TCT CCG GCT CCT GAA AAT CCC CAC TTC TGC CTC TCC CCT GAG CTG CTT CAT ATC AAG CCC
 ser pro ala pro glu asn pro his phe cys leu ser pro glu leu leu his ile lys pro
 1561/521 1591/531
 TAC CCG GAC CCC AGG GGC CGG CCC ACC AAG GAG ATT CTG GAG TTC CCC GCC CGC GAA GTC
 tyr pro asp pro arg gly arg pro thr lys glu ile leu glu phe pro ala arg glu val
 1621/541 1651/551
 TAT GCC CCC CAT ACC AGC TAC AGG AAC CTG CTG TAC GTG TAC CCG CAC AGC CTC AAC TTC
 tyr ala pro his thr ser tyr arg asn leu leu tyr val tyr pro his ser leu asn phe
 1681/561 1711/571
 AGC AGC CGC CAG GGC TCC GTG CGC AAC CTT GCT GTG CGA GTG CAG TAC ATG ACA GGC GAG
 ser ser arg gln gly ser val arg asn leu ala val arg val gln tyr met thr gly glu
 1741/581 1771/591
 GAC CCC AGC CAG GCT CTG CCG GTC ATC TTT GGC AAG TCC AGC TGC AGT GAA TTT ACC CGC
 asp pro ser gln ala leu pro val ile phe gly lys ser ser cys ser glu phe thr arg
 1801/601 1831/611
 GAG GCC TTC ACA CCG GTG GTC TAC CAT AAC AAG TCC CCC GAG TTC TAC GAG GAG TTC AAG
 glu ala phe thr pro val val tyr his asn lys ser pro glu phe tyr glu glu phe lys
 1861/621 1891/631
 CTG CAT CTT CCA GCC TGC GTG ACA GAG AAC CAT CAC CTG CTG TTC ACC TTC TAC CAT GTC
 leu his leu pro ala cys val thr glu asn his his leu leu phe thr phe tyr his val
 1921/641 1951/651
 AGC TGC CAG CCC CGG CCG GGC ACT GCC CTG GAG ACA CCC GTG GGC TTT ACT TGG ATC CCA
 ser cys gln pro arg pro gly thr ala leu glu thr pro val gly phe thr trp ile pro
 1981/661 2011/671
 CTG CTG CAG CAC GGG CGC CTG AGG ACC GGC CCC TTC TGT CTC CCA GTG TCT GTG GAC CAG
 leu leu gln his gly arg leu arg thr gly pro phe cys leu pro val ser val asp gln
 2041/681 2071/691
 CCG CCG CCC AGC TAT TCC GTG CTC ACA CCC GAT GTG GCG CTT CCG GGC ATG CGC TGG GTG
 pro pro pro ser tyr ser val leu thr pro asp val ala leu pro gly met arg trp val
 2101/701 2131/711
 GAC GGT CAC AAG GGC GTG TTC AGT GTG GAG CTC ACA GCC GTG TCC TCT GTG CAC CCC CAG
 asp gly his lys gly val phe ser val glu leu thr ala val ser ser val his pro gln
 2161/721 2191/731
 GAC CCC TAC CTG GAC AAA TTC TTC ACC CTG GTG CAC GTC CTG GAG GAG GGA GCC TTC CCA
 asp pro tyr leu asp lys phe phe thr leu val his val leu glu glu gly ala phe pro
 2221/741 2251/751
 TTC CGG CTC AAG GAC ACT GTG CTG AGC GAG GGC AAC GTG GAG CAG GAG CTG CGG GCC AGT
 phe arg leu lys asp thr val leu ser glu gly asn val glu gln glu leu arg ala ser
 2281/761 2311/771
 CTT GCA GCA CTG CGC CTG GCC AGC CCC GAA CCC CTT GTG GCC TTC TCC CAC CAC GTG CTG

leu ala ala leu arg leu ala ser pro glu pro leu val ala phe ser his his val leu
 2341/781 2371/791
 GAC AAG CTC GTG CGT CTG GTC ATC AGG CCC CCG ATC ATC AGT GGC CAG ATT GTG AAC CTG
 asp lys leu val arg leu val ile arg pro pro ile ile ser gly gln ile val asn leu
 2401/801 2431/811
 GGC CGT GGA GCC TTT GAA GCA ATG GCC CAT GTA GTC AGC CTT GTT CAC CGG AGC CTG GAG
 gly arg gly ala phe glu ala met ala his val val ser leu val his arg ser leu glu
 2461/821 2491/831
 GCA GCC CAG GAT GCC CGC GGT CAC TGC CCA CAG CTG GCT GCC TAC GTC CAC TAC GCC TTT
 ala ala gln asp ala arg gly his cys pro gln leu ala ala tyr val his tyr ala phe
 2521/841 2551/851
 CGC CTT CCT GGC ACT GAG CCC AGC CTC CCG GAT GGG GCC CCT CCA GTG ACA GTG CAG GCT
 arg leu pro gly thr glu pro ser leu pro asp gly ala pro pro val thr val gln ala
 2581/861 2611/871
 GCC ACA CTG GCC CGT GGC TCT GGT CGC CCC GCA AGC CTC TAC CTG GCG CGT TCC AAG AGC
 ala thr leu ala arg gly ser gly arg pro ala ser leu tyr leu ala arg ser lys ser
 2641/881 2671/891
 ATC AGC AGC AGC AAC CCT GAC CTC GCC GTG GCC CCT GGC TCT GTG GAT GAC GAG GTT TCC
 ile ser ser ser asn pro asp leu ala val ala pro gly ser val asp asp glu val ser
 2701/901 2731/911
 CGC ATC CTG GCC AGC AAG CTG CTT CAC GAG GAG CTG GCT CTG CAG TGG GTG GTC AGC AGC
 arg ile leu ala ser lys leu leu his glu glu leu ala leu gln trp val val ser ser
 2761/921 2791/931
 AGT GCC GTA CGC GAG GCC ATC CTC CAG CAC GCC TGG TTC TTC TTC CAG CTC ATG GTG AAG
 ser ala val arg glu ala ile leu gln his ala trp phe phe phe gln leu met val lys
 2821/941 2851/951
 AGT ATG GCG CTG CAC CTG CTG CTT GGC CAG CGA CTA GAC ACA CCC CGC AAG CTG CGC TTC
 ser met ala leu his leu leu leu gly gln arg leu asp thr pro arg lys leu arg phe
 2881/961 2911/971
 CCC GGA CGC TTC CTG GAC GAC ATC ACT GCC TTG GTG GGC TCT GTG GGC CTG GAG GTC ATC
 pro gly arg phe leu asp asp ile thr ala leu val gly ser val gly leu glu val ile
 2941/981 2971/991
 ACC CGT GTC CAC AAG GAT GTG GAG CTG GCC GAG CAC CTC AAC GCC AGC CTG GCT TTC TTC
 thr arg val his lys asp val glu leu ala glu his leu asn ala ser leu ala phe phe
 3001/1001 3031/1011
 CTC AGT GAC CTT CTG TCC CTG GTG GAC CGG GGC TTT GTC TTC AGC CTG GTC CGG GCC CAC
 leu ser asp leu leu ser leu val asp arg gly phe val phe ser leu val arg ala his
 3061/1021 3091/1031
 TAC AAG CAG GTG GCC ACG CGG CTC CAG TCG TCC CCT AAT CCA GCA GCC CTG CTG ACC CTG
 tyr lys gln val ala thr arg leu gln ser ser pro asn pro ala ala leu leu thr leu
 3121/1041 3151/1051
 CGC ATG GAA TTC ACC CGC ATC CTG TGC AGC CAC GAG CAC TAC GTG ACC CTC AAC CTC CCC
 arg met glu phe thr arg ile leu cys ser his glu his tyr val thr leu asn leu pro
 3181/1061 3211/1071
 TGC TGC CCC CTG TCA CCT CCA GCC TCG CCC TCC CCC TCT GTG TCC TCC ACC ACC TCC CAG
 cys cys pro leu ser pro pro ala ser pro ser pro ser val ser ser thr thr ser gln
 3241/1081 3271/1091
 AGC TCC ACC TTC TCC AGC CAA GCC CCG GAC CCC AAG GTG ACC AGC ATG TTC GAA CTG AGT
 ser ser thr phe ser ser gln ala pro asp pro lys val thr ser met phe glu leu ser
 3301/1101 3331/1111
 GGA CCA TTC CGG CAG CAG CAC TTC CTA GCT GGG CTC CTG CTG ACG GAG CTG GCA CTG GCC
 gly pro phe arg gln gln his phe leu ala gly leu leu leu thr glu leu ala leu ala
 3361/1121 3391/1131
 CTC GAA CCT GAG GCT GAA GGG GCA TTC CTG TTG CAC AAG AAG GCC ATC AGT GCT GTG CAC
 leu glu pro glu ala glu gly ala phe leu leu his lys lys ala ile ser ala val his
 3421/1141 3451/1151
 AGC CTG CTA TGT GGC CAT GAC ACT GAC CCC CGC TAC GCC GAG GCC ACT GTG AAG GCT CGT
 ser leu leu cys gly his asp thr asp pro arg tyr ala glu ala thr val lys ala arg
 3481/1161 3511/1171
 GTG GCC GAG CTG TAC CTG CCA CTG CTT TCG ATT GCA CGG GAT ACC TTG CCA CGG CTG CAT
 val ala glu leu tyr leu pro leu leu ser ile ala arg asp thr leu pro arg leu his

3541/1181	GAC TTT GCT GAG GGC CCA GGT CAG CGG TCA	3571/1191	AGA CTG GCC TCA ATG CTT GAC TCA GAC ACA
asp phe ala glu gly pro gly gln arg ser		arg leu ala ser met leu asp ser asp thr	
3601/1201	GAA GGC GAA GGG GAC ATT GCG GGT ACC ATC	3631/1211	AAC CCC TCT GTG GCC ATG GCC ATT GCT GGT
glu gly glu gly asp ile ala gly thr ile		asn pro ser val ala met ala ile ala gly	
3661/1221	GGC CCC CTA GCC CCT GGC TCC CGG GCC AGC	3691/1231	ATC TCC CAG GGG CCA CCA ACG GCT TCT CGC
gly pro leu ala pro gly ser arg ala ser		ile ser gln gly pro pro thr ala ser arg	
3721/1241	GCA GGC TGT GCC CTC TCT GCT GAG TCA AGC	3751/1251	CGG ACC TTG CTG GCG TGT GTG CTG TGG GTG
ala gly cys ala leu ser ala glu ser ser		arg thr leu leu ala cys val leu trp val	
3781/1261	CTG AAA AAC ACC GAG CCG GCG CTC CTG CAG	3811/1271	CGC TGG GCC ACT GAC CTG ACA CTC CCC CAG
leu lys asn thr glu pro ala leu leu gln		arg trp ala thr asp leu thr leu pro gln	
3841/1281	CTG GGA CGT CTG TTG GAC TTG CTG TAC CTT	3871/1291	TGC CTG GCT GCC TTT GAG TAC AAG GGG AAA
leu gly arg leu leu asp leu leu tyr leu		cys leu ala ala phe glu tyr lys gly lys	
3901/1301	AAG GCC TTT GAA CGC ATC AAC AGC CTC ACA	3931/1311	TTC AAA AAA TCT CTG GAT ATG AAG GCG CGG
lys ala phe glu arg ile asn ser leu thr		phe lys lys ser leu asp met lys ala arg	
3961/1321	CTA GAG GAA GCC ATT CTG GGT ACC ATC GGA	3991/1331	GCT CGA CAA GAA ATG GTT CGG CGA AGT CGT
leu glu glu ala ile leu gly thr ile gly		ala arg gln glu met val arg arg ser arg	
4021/1341	GAG AGG AGC CCG TTT GGG AAT CCA GAG AAC	4051/1351	GTG CGC TGG CGG AAG AGC GTC ACA CAC TGG
glu arg ser pro phe gly asn pro glu asn		val arg trp arg lys ser val thr his trp	
4081/1361	AAG CAA ACC TCA GAC CGC GTG GAC AAG ACC	4111/1371	AAG GAT GAA ATG GAA CAC GAG GCC TTG GTG
lys gln thr ser asp arg val asp lys thr		lys asp glu met glu his glu ala leu val	
4141/1381	GAA GGG AAC CTG GCA ACC GAG GCA AGC CTA	4171/1391	GTG GTT CTG GAC ACA CTG GAG ATC ATC GTG
glu gly asn leu ala thr glu ala ser leu		val val leu asp thr leu glu ile ile val	
4201/1401	CAG ACG GTG ATG CTT TCA GAA GCC CGG GAG	4231/1411	AGC GTC TTG GGG GCA GTG CTG AAG GTT GTG
gln thr val met leu ser glu ala arg glu		ser val leu gly ala val leu lys val val	
4261/1421	CTG TAC AGC CTG GGC AGT GCC CAG AGT GCC	4291/1431	CTC TTC TTG CAG CAT GGC CTG GCC ACC CAG
leu tyr ser leu gly ser ala gln ser ala		leu phe leu gln his gly leu ala thr gln	
4321/1441	AGG GCC CTT GTG TCC AAG TTC CCG GAG CTG	4351/1451	CTG TTC GAG GAG GAC ACG GAG CTG TGT GCC
arg ala leu val ser lys phe pro glu leu		leu phe glu glu asp thr glu leu cys ala	
4381/1461	GAC CTG TGC CTG AGG CTC CTA CGA CAC TGT	4411/1471	GGC AGC CGC ATC AGC ACC ATC CGC ACG CAC
asp leu cys leu arg leu leu arg his cys		gly ser arg ile ser thr ile arg thr his	
4441/1481	GCC AGC GCC TCG CTG TAC CTG CTC ATG CGA	4471/1491	CAG AAC TTC GAG ATC GGC CAC AAC TTT GCC
ala ser ala ser leu tyr leu leu met arg		gln asn phe glu ile gly his asn phe ala	
4501/1501	CGT GTG AAG ATG CAG GTC ACC ATG TCT CTC	4531/1511	TCG TCC CTG GTG GGG ACG ACG CAG AAC TTC
arg val lys met gln val thr met ser leu		ser ser leu val gly thr thr gln asn phe	
4561/1521	AGT GAA GAG CAC CTG CGA CGT TCA CTC AAA	4591/1531	ACC ATC CTC ACC TAT GCT GAG GAG GAC ATG
ser glu glu his leu arg arg ser leu lys		thr ile leu thr tyr ala glu glu asp met	
4621/1541	GGG CTG CGG GAC AGC ACC TTC GCA GAG CAG	4651/1551	GTC CAG GAC CTG ATG TTC AAC CTG CAC ATG
gly leu arg asp ser thr phe ala glu gln		val gln asp leu met phe asn leu his met	
4681/1561	ATC CTG ACG GAC ACG GTG AAG ATG AAG GAA	4711/1571	CAC CAG GAG GAC CCT GAG ATG CTC ATC GAC
ile leu thr asp thr val lys met lys glu		his gln glu asp pro glu met leu ile asp	
4741/1581		4771/1591	

CTC ATG TAC AGA ATT GCC CGG GGC TAC CAG GGC TCA CCG GAC CTT CGG CTG ACC TGG TTG
 leu met tyr arg ile ala arg gly tyr gln gly ser pro asp leu arg leu thr trp leu
 4801/1601 4831/1611
 CAG AAC ATG GCC GGG AAG CAC GCG GAG CTG GGC AAC CAC GCC GAG GCC GCC CAG TGC ATG
 gln asn met ala gly lys his ala glu leu gly asn his ala glu ala ala gln cys met
 4861/1621 4891/1631
 GTG CAC GCG GCC GCC CTC GTG GCT GAG TAC CTC GCC CTG CTC GAG GAC CAG CGC CAC CTG
 val his ala ala ala leu val ala glu tyr leu ala leu leu glu asp gln arg his leu
 4921/1641 4951/1651
 CCC GTG GGC TGC GTT TCC TTC CAG AAC ATC TCA TCC AAC GTG CTA GAG GAG TCC GCC ATC
 pro val gly cys val ser phe gln asn ile ser ser asn val leu glu glu ser ala ile
 4981/1661 5011/1671
 TCC GAC GAC ATC CTG TCG CCC GAC GAG GAG GGC TTC TGC TCC GGG AAG CAC TTC ACT GAG
 ser asp asp ile leu ser pro asp glu glu gly phe cys ser gly lys his phe thr glu
 5041/1681 5071/1691
 CTG GGG CTG GTA GGG TTG CTG GAA CAG GCA GCC GGC TAC TTC ACC ATG GGC GGG CTC TAC
 leu gly leu val gly leu leu glu gln ala ala gly tyr phe thr met gly gly leu tyr
 5101/1701 5131/1711
 GAG GCG GTG AAT GAG GTC TAC AAG AAC CTC ATC CCC ATC CTG GAA GCC CAC CGT GAC TAC
 glu ala val asn glu val tyr lys asn leu ile pro ile leu glu ala his arg asp tyr
 5161/1721 5191/1731
 AAG AAG CTG GCC GCG GTG CAC GGC AAA CTG CAG GAG GCC TTC ACC AAG ATC ATG CAC CAG
 lys lys leu ala ala val his gly lys leu gln glu ala phe thr lys ile met his gln
 5221/1741 5251/1751
 AGT TCC GGC TGG GAG CGC GTG TTC GGG ACG TAT TTC CGC GTG GGC TTC TAC GGC GCC CAC
 ser ser gly trp glu arg val phe gly thr tyr phe arg val gly phe tyr gly ala his
 5281/1761 5311/1771
 TTC GGT GAC CTG GAT GAG CAG GAG TTT GTG TAC AAG GAG CCA TCG ATC ACG AAG CTG GCA
 phe gly asp leu asp glu gln glu phe val tyr lys glu pro ser ile thr lys leu ala
 5341/1781 5371/1791
 GAG ATC TCA CAC CGG CTG GAG GAG TTC TAC ACG GAG AGA TTT GGC GAC GAC GTC GTT GAG
 glu ile ser his arg leu glu glu phe tyr thr glu arg phe gly asp asp val val glu
 5401/1801 5431/1811
 ATT ATC AAA GAC TCT TAC CCT GTG GAC AAG TCC AAG CTT GAC TCA CAA AAG GCC TAC ATC
 ile ile lys asp ser tyr pro val asp lys ser lys leu asp ser gln lys ala tyr ile
 5461/1821 5491/1831
 CAG ATC ACG TAT GTG GAA CCG TAC TTT GAT ACC TAC GAG CTC AAG GAC CGG GTG ACC TAC
 gln ile thr tyr val glu pro tyr phe asp thr tyr glu leu lys asp arg val thr tyr
 5521/1841 5551/1851
 TTT GAC CGC AAC TAT GGG CTT CGC ACA TTC CTG TTC TGC ACG CCG TTC ACG CCG GAT GGG
 phe asp arg asn tyr gly leu arg thr phe leu phe cys thr pro phe thr pro asp gly
 5581/1861 5611/1871
 CGC GCA CAC GGG GAG CTG CCC GAG CAA CAC AAG CGT AAG ACG CTG CTC AGC ACC GAC CAC
 arg ala his gly glu leu pro glu gln his lys arg lys thr leu leu ser thr asp his
 5641/1881 5671/1891
 GCC TTC CCC TAC ATC AAG ACT CGC ATC CGT GTG TGC CAC CGG GAG GAG ACG GTG CTG ACG
 ala phe pro tyr ile lys thr arg ile arg val cys his arg glu glu thr val leu thr
 5701/1901 5731/1911
 CCA GTG GAG GTG GCC ATC GAG GAC ATG CAG AAG AAG ACA CGG GAG CTG GCC TTT GCC ACC
 pro val glu val ala ile glu asp met gln lys lys thr arg glu leu ala phe ala thr
 5761/1921 5791/1931
 GAG CAG GAC CCA CCA GAT GCT AAG ATG CTA CAG ATG GTG CTT CAG GGC TCT GTA GGG CCC
 glu gln asp pro pro asp ala lys met leu gln met val leu gln gly ser val gly pro
 5821/1941 5851/1951
 ACC GTG AAC CAG GGT CCC CTG GAG GTG GCC CAG GTG TTT TTA GCA GAG ATC CCG GAA GAC
 thr val asn gln gly pro leu glu val ala gln val phe leu ala glu ile pro glu asp
 5881/1961 5911/1971
 CCC AAG CTC TTC CGG CAT CAC AAC AAA TTG CGG CTC TGC TTC AAG GAC TTC TGC AAG AAA
 pro lys leu phe arg his his asn lys leu arg leu cys phe lys asp phe cys lys lys
 5941/1981 5971/1991
 TGT GAG GAT GCG CTG CGG AAA AAT AAG GCC CTG ATT GGG CCG GAC CAG AAG GAG TAC CAC

cys glu asp ala leu arg lys asn lys ala leu ile gly pro asp gln lys glu tyr his
 6001/2001 6031/2011
 CGT GAG CTG GAG CGC AAC TAC TGC CGC CTG CGG GAG GCT CTG CAG CCC CTG CTT ACC CAG
 arg glu leu glu arg asn tyr cys arg leu arg glu ala leu gln pro leu leu thr gln
 6061/2021 6091/2031
 CGC CTG CCC CAG CTG ATG GCA CCC ACC CCA CCC GGC CTC AGG AAC TCC TTG AAC AGA GCA
 arg leu pro gln leu met ala pro thr pro pro gly leu arg asn ser leu asn arg ala
 6121/2041 6151/2051
 AGT TTC CGA AAG GCA GAC CTC TGA GCC CAC AAG GAC CAA AGC TGT ACC TAG AGG AAC CAG
 ser phe arg lys ala asp leu OPA
 6181/2061 6211/2071
 CAC CCG GGC CTC AGC TGT CTG TGC TGC GAG GGG AGT CTG CCC TGG TGC CCA CTG GGC TGT
 6241/2081 6271/2091
 GGG GTG ACC ACA CTG TAC TTG GGG CTG GGC CCT CTG CCC CTG TGT CCC CAT CTG TGT GCA
 6301/2101 6331/2111
 CTG ATG CTT CCT CCC TTT TTT AAT TTA AAA TGG TTT TTA TAA GCA AAA AAA AAA AAA AAA

6001/2001
 6031/2011
 6061/2021
 6091/2031
 6121/2041
 6151/2051
 6181/2061
 6211/2071
 6241/2081
 6271/2091
 6301/2101
 6331/2111

A. Allelic variations: single nucleotide changes (polymorphism) between CLASP-7 cDNA isoforms

Isoform	Nucleotide(s)	Consequence
1	1993	G to A; glycine to arginine
2	2136	A to G; missense
3	3166	A to G; threonine to alanine
4	3902	A to T; lysine to methionine
5	3918	C to T; missense
6	3937	A to C; lysine to glutamine
7	4002	A to C; glutamic acid to aspartic acid
8	4017	T to A; serine to arginine
9	4020	T to C; missense
10	4034-5	TT to AC; phenylalanine to tyrosine
11	4911	G to C change; missense mutation changing codon from glutamine to histidine

These differences may be found separately or together in various combination in the difference human CLASP-7 isoforms

FIG. 5

B

The diagram illustrates a DNA probe with a 3' end at position -12 and a 5' end at position 6360. A specific region of the DNA, spanning from position 4213 to 4945, is highlighted. This region is divided into three sub-regions labeled i, ii, and iii. Region i is located between positions 4213 and 4945. Region ii is located between positions 4945 and 6360. Region iii is located between positions 4213 and 4945. The DNA sequence is represented by a horizontal line with vertical tick marks indicating the positions of the labels.

C

FIG. 5

CLASP-7 intron/exons

Exon 63800 to 63920

GCGGGGCGGGGGCCCGGGGCGGCGGCGGGGACGCGAGGACCATGGCTGC
CTCCGAGCGCCGCGCCTTCGCGCACAAAGATCAACAGGTAGTGTGGCCGCGGG
GCCCCCTCCACCTCCC

Exon 72530 to 72670

CCAATGGCCCCCTCCCTATCTTTCCAGGACGGTGGCCGCAGAGGTGCGGAAG
CAGGTGTCCCGGGAACGCAGTGGCTCCCCCCTCCAGCAGGCGCTGCAGCA
GCTCCCTGGGGGTAAAGTATTTGGGGGGTCCGCCCCCA

Exon 73300 to 73530

TCACAGCCACTTTGCTCCAATCCAGGTCCCCTGACTGAAGTTGTCGAGCCCC
TGGACTTTGAGGATGTACTTCTGAGCCGGCCACCAGATGCTGAGCCCGGGCC
CCTCAGGGACCTGGTAGAATTCCCAGCTGATGACTTGGAGCTGCTGCTGCAG
CCCCGGGAATGCCGGACCACGGAGCCCGGGATCCCCAAGGATGAGTGGGTTC
AGCCCCACGCCCTCTCTGCCTG

Exon 73700 to 73830

GTCTCTGTTTACCCTGATCTTCTTTTGTCTGCAGAAACTGGATGCCCAGGTGA
GGGCCGCGGTGGAGATGTATATTGAGGACTGGGTTCATTGTCCACAGAAGGTG
AGTCTGACTTAGGGGCAGCTCAGGGG

Exon 74010 to 74190

CCTGCCCAGCCCCGTTTCCTGCTAGGTATCAGTACCTGAGTGCAGCATAACAGC
CCCGTCACCACAGACACACAGCGGGAGCGACAGAAGGGCCTCCCCCGCCAG
GTCTTTGAGCAGGATGCTTCTGGAGACGAGAGGTCCGGGCCCTGAGGACTCGG
TGAGGAAGCCCCTGGCTGGGGTCAC

Exon 75170 to 75450

CAGTGCTTGCACATTCTCCACTGGCAGAAATGACTCCCGGCGTGGCTCGGGCTC
CCCGGAAGACACCCCTCGAAGCAGTGGTGCCTCTAGCATCTTCGACCTGAGG
AACCTGGCAGCTGACTCATTGCTGCCCTCTCTGCTAGAGCGGGCGGCCCCAG
AAGATGTGGACCGGCGCAATGAAACCCTTCGACGGCAGCACCGGCCCCCGGC
CCTGCTCACCCCTCTACCCGGCACCTGACGAGGTGGGTGCCCCTTCCAGATAT
CAGCCAACCAGCATTACT

Exon 78100 to 78250

CCCGCCCAGCTCCCACCCCCCACTCTTGGCAGGATGAAGCCGTGGAACGCTG
TAGCCGCCAGAGCCACCCCGCGAGCACTTTGGACAAAGGATCTTGGTCAAG
TGTCTGTCGCTCAAGTGAGTATACTGACATGTCTCTCTTCTTAGATG

Exon 80380 to 80500

CCCCCTCCCTCCCATTTACTTGTAGGTTTCGAGATTGAAATTGAGCCCATCTTT
GGGATCTTGGCTCTGTATGATGTGCGGGAGAAAAAGAAGGTAGGAGGCCCTT
TTTTCTCTTTCCTCCC

Exon 80540 to 80750

GTGGTGGCCCAGCTGCCTCTGGTGTCCCCAGATCTCGGAGAACTTCTACTTCG
ACCTGAACTCGGACTCCATGAAGGGGCTGCTTCGGGCTCATGGCACCCACCC
TGCCATCTCCACCCTGGCCCGCTCTGCCATCTTCTCTGTGACCTACCCCTCACC
TGACATCTTCCTGGTCATCAAGGTGCCTGCTGGGGCTGGGCAAGGGGGTGGT

Exon 82370 to 82510

GCCTCACTGGATTCAATTCATCTGCCCCGCAGTTGGAGAAGGTGCTTCAGCAAG
GGGACATCAGTGAGTGCTGTGAGCCTTACATGGTGTGAAAGAAGTGGACAC
AGCCAAGGTAAGCGTGTGGAGGCTGGACTAGGGGCA

Exon 82540 to 82760

GCTGAGCTGGCAGGGGACGGGGTCTCCCCACAGAACAAAGAGAAGCTAGAG
AAGCTGCGCCTGGCGGCCGAGCAGTTCTGCACCCGCCTGGGCGCTACCGCA
TGCCCTTCGCCTGGACGGCCGTGCACTTGGCCAACATCGTGAGCAGCGCTGG
GCAGCTGGACCGGGACTCTGACTCGGAGGGCGGTGAGGAGGCGGGGCTAAC
AGGCTTGGGGCGGGG

Exon 82860 to 83060

CTTGGTCCCCCTTTTGTCAATTGTCATTCCCTCCCCTAGAGCGCCGGCCAGCCT
GGACAGACCGCCGCGGTCGGGGGGCCCCAGGACCGGGCGAGTAGTGGGGACG
ACGCCTGCAGCTTCTCTGGCTTCCGTCCAGCCACGCTAACTGTCACAACTTC
TTTAAGCAGGTGTCCTACCCTGGGGCCAGGGACTCTCCCACTCC

Exon 83100 to 83260

GCCCAGGCTGACGGGAGTGGGTCCCATGTAGGAGGCTGAGCGACTCAGTGAC
GAGGACCTCTTCAAGTTCCTGGCTGACATGAGGCGCCCGTCGTCCCTGCTGCG
GCGACTACGTCCTGTGACTGGTGCCTGGCACACCCCATACACAAGAAGTATC
ACTC

Exon 84050 to 84270

GTGCAAACCGGTTCTTCCCTTCCCAGCCCAGCTCAAGATCGACATTTCTCCGG
CTCCTGAAAATCCCCACTTCTGCCTCTCCCCTGAGCTGCTTCATATCAAGCCC
TACCCGGACCCCAGGGGCGGCCACCAAGGAGATTCTGGAGTTCCCCGCC
GCGAAGTCTATGCCCCCATACCAGCTACAGGTACGGCCTCTGGGGCCCAGC
TGGGCACTTGA

Exon 87940 to 88130

GCCCCTGTCCCTCTGACACCCCCATCCTGCCCCCACAGGAACCTGCTGTACG
TGTACCCGCACAGCCTCAACTTCAGCAGCCGCCAGGGCTCCGTGCGCAACCT
TGCTGTGCGAGTGCAGTACATGACAGGCGAGGACCCCAGCCAGGCTCTGCCG
GTCAGTGGCTGTGCCCCAGGGAAGGGGGGTAGGG

Exon 88140 to 88270

TGGGTCCCTCATGAATCCACTCTCCCAGGTCATCTTTGGCAAGTCCAGCTGCA
GTGAATTTACCCGCGAGGCCTTCACACCGGTGGTCTACCATAACAAGTATGT
AGGGGGACACGTGAGGAACTTGGGGG

Exon 88470 to 88680

GCCCCCAGCAGATCCCCCAGCCCGATTCTGCCAGGTCCCCCGAGTTCTACGA
GGAGTTCAAGCTGCATCTTCCAGCCTGCGTGACAGAGAACCATCACCTGCTG
TTACCTTCTACCATGTCAGCTGCCAGCCCCGGCCGGGCACTGCCCTGGAGAC
ACCCGTGGGCTTTACTGTGAGCCGTCCCCTCCCTCCCTCCCCCTGAGCCCTCC
T

Exon 88680 to 88870

TCGTCCCCCAACCTGGCCGCAGACCTGACCTCCAGCCTCTCCCCAGTGGATCC
CACTGCTGCAGCACGGGCGCCTGAGGACCGGCCCTTCTGTCTCCCAGTGTCT
GTGGACCAGCCGCCGCCAGCTATTCCGTGCTCACACCCGATGTATGTGCCCT
GGAGCTCCTGCCTGCCAATGCACTGTCCCCAG

Exon 89360 to 89530

CAGGGAGGGCTGACCAGTGCCACCTGGTGCCTCCCTCCCACAGGTGGCGCT
TCCGGGCATGCGCTGGGTGGACGGTCACAAGGGCGTGTTCAAGTGTGGAGCTC
ACAGCCGTGTCCTCTGTGCACCCCCAGGTACGGGGTGGGCCGGGAACCAAGA
GTCCCGCCCTGCTCC

Exon 89660 to 89980

TTCATTCCCTGAGGCCCCACCCTGCTCACTCCACATCCCTACCCAGGACCCCT
ACCTGGACAAATTCTTCACCCTGGTGCACGTCCTGGAGGAGGGAGCCTTCCC
ATTCCGGCTCAAGGACACTGTGCTGAGCGAGGGCAACGTGGAGCAGGAGCTG
CGGGCCAGTCTTGACGACTGCGCCTGGCCAGCCCCGAACCCCTTGTGGCCTT
CTCCCACCACGTGCTGGACAAGCTCGTGCGTCTGGTCATCAGGCCCCCGATC
ATCAGTGGCCAGATTGGTAAGCGAATGTGGCCTCAGACCTCAGTTTCCCCATC
CACATG

Exon 90480 to 90730

AGAGGCCTTGGGGCCCTGGAACCTTGACCTCTGCTCTGCCCTGCAGTGAACCTG
GGCCGTGGAGCCTTTGAAGCAATGGCCCATGTAGTCAGCCTTGTTCACCGGA
GCCTGGAGGCAGCCAGGATGCCCGCGGTCACTGCCACAGCTGGCTGCCTA
CGTCCACTACGCCTTTCGCCTTCTGGCACTGAGCCCAGCCTCCCGGATGGTG
AGTTTGTAGAAATCCCTGTGAGACGAGAAATATCTGGGAGAA

Exon 92870 to 93120

ATCACATCAGGTGGGTGGGTGGTTGACCCTATTCCTCCATCCTCAGGGGCCC
CTCCAGTGACAGTGCAGGCTGCCACACTGGCCCGTGGCTCTGGTCGCCCCGC
AAGCCTCTACCTGGCGCGTTCCAAGAGCATCAGCAGCAGCAACCCTGACCTC
GCCGTGGCCCCTGGCTCTGTGGATGACGAGGTTTCCCGCATCCTGGCCAGCA
AGGTAGGGCAACGGGGGCCCTGGAATCTCCAGCCTCAGTGGT

Exon 97210 to 97390

GGCACCTCGCACTCTGTGACCCCTGCCTCTGTCCCCAGCTGCTTCACGAGGAG
CTGGCTCTGCAGTGGGTGGTCAGCAGCAGTGCCGTACGCGAGGCCATCCTCC
AGCACGCCTGGTTCTTCTCCAGCTCATGGTGAGACCCCTCCTCCCTGCCTG
GTGGCAAGAGACCCCCAGTGGAG

Exon 98770 to 98990

CAAATCCCACCCACAGCCCTCTACCCCCACCCCCAGGTGAAGAGTATGGCGC
TGCACCTGCTGCTTGGCCAGCGACTAGACACACCCCGCAAGCTGCGCTTCCC
CGGACGCTTCCTGGACGACATCACTGCCTTGGTGGGCTCTGTGGGCCTGGAG
GTCATACCCGTGTCCACAAGGTGAGAGATGCAGGGTCTCAATGTGGGAAGA
AACCTGAGGGAGG

Exon 103130 to 103340

GGGGCTGAGGTTTGGGTGTGTGGGTGACAGGCACCTGTGTCCCCAGGATGT
GGAGCTGGCCGAGCACCTCAACGCCAGCCTGGCTTTCTTCCTCAGTGACCTTC
TGTCCCTGGTGGACCGGGGCTTTGTCTTCAGCCTGGTCCGGGGCCCACTACAAG
CAGGTAGGAGTGGGCGTGGGCAGGGTGGGCATGGCATGGATGGAAGGCGGA
GC

Exon 103340 to 103590

CAATGTTGACATCACTGATGGCCACCCCTCTCCTGCAGGTGGCCACGCGGCTC
CAGTCGTCCCCTAATCCAGCAGCCCTGCTGACCCTGCGCATGGAATTCACCCG
CATCCTGTGCAGCCACGAGCACTACGTGACCCTCAACCTCCCCTGCTGCCCCC
TGTACCTCCAGCCTCGCCCTCCCCCTCTGTGTCCTCCACCACCTCCCAGGTG
GGCTGCCTTCACTTCTGCCTCCTCTCTTTGACCTACAAC

Exon 103990 to 104220

TGACCCTTGACCGCTGGCATCCCCCATTTTTCCCCCACTCTGCAGAGCTCCAC
CTTCTCCAGCCAAGCCCCGGACCCCAAGGTGACCAGCATGTTCGAACTGAGT
GGACCATTCGGGAGCAGCACTTCCTAGCTGGGCTCCTGCTGACGGAGCTGG
CACTGGCCCTCGAACCTGAGGCTGAAGGGTGAGCAGAGCTCCTGTCTAGCCC
CAGGACAGGTGGGACAGTCCAG

Exon 104220 to 104480

GGAGCCATGTCCACCCTGTCCTGAGCACCTCATTACCCCATAGGGCATTCCCTG
TTGCACAAGAAGGCCATCAGTGCTGTGCACAGCCTGCTATGTGGCCATGACA
CTGACCCCCGCTACGCCGAGGCCACTGTGAAGGCTCGTGTGGCCGAGCTGTA
CCTGCCACTGCTATCGATTGCACGGGATACCTTGCCACGGCTGCATGACTTIG
CTGGTCAGTGGGCCAGGGGAAGATGGGGTCACATGATCCAGGGACTTGGTC

Exon 108850 to 109100

ACCAAGGGTTTATCTTTCTTTCCCTCTGTCTTTCCCTGCCAGAGGGGCCAGGTC
AGCGGTCAAGACTGGCCTCAATGCTTGACTCAGACACAGAAGGCGAAGGGG
ACATTGCGGGTACCATCAACCCCTCTGTGGCCATGGCCATTGCTGGTGGCCCC
CTAGCCCCTGGCTCCCGGGCCAGCATCTCCAGGGGGCCACCAACGGTGAGTA
GGGAGGCTTGTCCCCATAGACATCATCCACTTTGAATGAGA

Exon 109140 to 109410

TCACATGGAGAAAATGGAAATTGACTTTGATTCTCTCTGGCCCCAGGCTTCT
CGCGCAGGCTGTGCCCTCTCTGCTGAGTCAAGCCGGACCTTGCTGGCGTGTGT
GCTGTGGGTGCTGAAAAACACCGAGCCGGCGCTCCTGCAGCGCTGGGCCACT
GACCTGACACTCCCCAGCTGGGACGTCTGTTGGATTGCTGTACCTTTGCCT
AGCTGCCTTTGAGTACAAGGTTTGAGGGCGTGGGCAGGAGATGATGGAGGAG
GCAGGCTA

Exon 110310 to 110530

GAAAAGAGCAGAGTCAGCCTGGAACCCCAGTTCTCTGCACCCCCAGGGGAA
AAAGGCCTTTGAACGCATCAACAGCCTCACATTCAAAAAATCTCTGGATATG
AAGGCGCGGCTAGAGGAAGCCATTCTGGGTACCATCGGAGCTCGACAAGAA
ATGGTTCGGCGAAGTCGTGGTAAGAGGGTGACATACCCACGTGTCCCCATCC
CACCAGCTGCTCCA

Exon 110770 to 110940

TGTGTTTTTACGCATCTGTGATCGTGCACCCACGCGTCTCAGAGAGGAGCCCG
TTTGGGAATCCGGAGAATGTGCGCTGGCGGAAGAGCGTCACACACTGGAAGC
AAACCTCAGACCGCGTGGACAAGTAGGTGTGGGCAGGAGGGTGTCTGCTGAG
TTCAGAACAGTTTG

Exon 111590 to 111770

ATCTCACCCCGAGTGGGCCCCCAAGACCTCCTTTCCCCTTCCAGGACCAAGG
ATGAAATGGAACACGAGGCCTTGGTGGAAGGGAACCTGGCAACCGAGGCAA
GCCTAGTGGTTCTGGACACACTGGAGATCATCGTGCAGGTAGGGCTTGATCC
AGCATCTGCCTTGTGCTCTGAGCCCA

Exon 111830 to 112050

ACCCTAGGCTCTAACACCTGGATTTCTGACCCCTTCCCTCCAGACGGTGATG
CTTTCAGAAAGCCCGGGAGAGCGTCTTGGGGGCAGTGCTGAAGGTTGTGCTGT
ACAGCCTGGGCAGTGCCAGAGTGCCCTCTTCTTGCAGCATGGCCTGGCCAC
CCAGAGGGCCCTTGTGTCCAAGGTGAGCACCCTCAACAACCATGATTCTTA
GAAAAACAGTAG

Exon 112910 to 113140

AACGGGGAGGGGCTGGACAGTGTCTGTCTGGGTCCTTGGGGGCAGTTCCCGG
AGCTGCTGTTTCGAGGAGGACACGGAGCTGTGTGCCGACCTGTGCCTGAGGCT
CCTACGACACTGTGGCAGCCGCATCAGCACCATCCGCACGCACGCCAGCGCC
TCGCTGTACCTGCTCATGCGACAGAACTTCGAGATCGGCCACGTGAGTGGGG
GCTAGGAGGCATGGTCCACACATGGCTCTGGTC

Exon 114090 to 114340

TCTGAGACTCCCGGCTCCACCCTCCCGCCCCTGTCCCTGCAGAACTTTGCCCCG
TGTGAAGATGCAGGTACCATGTCTCTCTCGTCCCTGGTGGGGACGACGCAG
AACTTCAGTGAAGAGCACCTGCGACGTTCACTCAAAACCATCCTCACCTATG
CTGAGGAGGACATGGGGCTGCGGGACAGCACCTTCGCAGAGCAGGTGACAC
CTGCTGGGTCCCCGCCCCGCCTCCCCTTCATATAACTCCCAAC

Exon 114370 to 114550

ATGCTCTCATTGGCCCCCTGGACGTTCCCCGGCTCCAGGTCCAGGACCTGATGT
TCAACCTGCACATGATCCTGACGGACACGGTGAAGATGAAGGAACACCAGG
AGGACCCTGAGATGCTCATCGACCTCATGTACAGGTGAGGTGGGCCAGCTGG
CACCTTCAGCCACGCCACGCCCA

Exon 116900 to 117170

AGGTGAGTCCCCTCCTCACATCCCCCCTCACCTGGACTCCAGAATTGCCCCGGG
GCTACCAGGGGCTCACCGGACCTTCGGCTGACCTGGTTGCAGAACATGGCCGG
GAAGCACGCGGACGTGGGCAACCACGCCGAGGCCGCCAGTGCATGGTGCA
CGCGGCCGCCCTCGTGGCTGAGTACCTCGCCCTGCTCGAGGACCAGCGCCAC
CTGCCCCGTGGCTGGCGATTTCTTCCAGGTGAGTGGCCAGGGGTGGCAGGT
GGCGGACGGCA

Exon 117170 to 117410

ACGAGTGCAGTGGGGACCAGGGTCTGACGCCACCTCTCCCACCCAGAACAT
CTCATCCAACGTGCTAGAGGAGTCCGCCATCTCCGACGACATCCTGTCGCCC
GACGAGGAGGGCTTCTGCTCCGGGAAGCACTTCACTGAGCTGGGGCTGGTAG
GGTTGCTGGAACAGGCAGCCGGCTACTTCACCATGGTGAGGCCTTGGGGACT
GGGTGCAGGAGAGGGGGCTCGGGCCAGGGAGGT

Exon 121670 to 121900

GAGAGGAAGACAGTTTGGGGAATCCTGACCCACCTCACCTCAGGGCGGGC
TCTACGAGGCGGTGAATGAGGTCTACAAGAACCTCATCCCCATCCTGGAAGC
CCACCGTGACTACAAGAAGCTGGCCGCGGTGCACGGCAAACCTGCAGGAGGC
CTTCACCAAGATCATGCACCAGGTGGGCCCAGGACCCCTCCCCAGACCCCA
CCCTCAGCCCCACTCCTCATCC

Exon 121910 to 122000

CCCCAGGGATCTGCTGACCTTGACCCTTCTCTTCCCCACAGAGTTCCGGCTGG
GAGGTGAGTCAGCCTTGGTGGACAGCCACCTGCCTCTG

Exon 123290 to 123510

TCCAGCAGGGGCCTCCCGGACAACCACACCCTTTCTCACAGCCCCAGCGCGT
GTTCGGGACGTATTTCCGCGTGGGCTTCTACGGCGCCCACTTCGGTGACCTGG
ATGAGCAGGAGTTTGTGTACAAGGAGCCATCGATCACGAAGCTGGCAGAGAT
CTCACACCGGCTGGAGGCATGTCCTTGTGGTTGGGGGTGGAACGGGGCATGG
GGCTGCCTTGGG

Exon 123510 to 123633 (end clone)

GGCTGGAGTAGGGGCTGTCCCTGGGTGGCCCCGAGTCAGCCCTGTGTCTCCA
GGAGTTCTACACGGAGAGATTTGGCGACGACGTCGTTGAGATTATCAAAGAC
TCTAACCTGTGGACAAGTC

Human CLASP-7 promoter region , 61938 (beginning of contig) to 63888 (end of first predicted exon)

GGGCATGTGGCTCATTCCTGTAATCCCGGCACTTTGGGAGGCCGAGGCGGGTGGATC
ACCTGAGGTGAGGAGCTCCAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTAC
TAAAAATACAAAAAATTAGCCAGGTGTGATGGTGGGTGCCTGTAATCCCAGCTACTC
GGGAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGCAGAGGTTGCGGTGAGCC
GAGATTGTGCCATTGCACTCCAGTCTGGGCAACAAGAGCGAAATGCCACCTCAAAAT
AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAGAGGATAA
AATGCCAGCAACCCATAGATGGGAATGAGAACAGCACGTGCAAAGGCCCTGAGGCA
GAGCCACGGCCTTGTCTGATTCAACCTCAAATTCTCCCTGGGGCATTGTGCTGACCAGG
GAAAGAAGGGCTGTCCAGGAGGAAGGACCTGCCGGTGCAGAGGCATGCAGGTGAGA
AAGGGGTGAGCTCCTCCAGAGGGGAGTGTGCGCTGGAGAATTCTCTAAAAATGCTGC
AGCAGTGCTGGGAGAGAGGCCAGTGGGGAGAGATTGAGACCATAGATTAACCAAG
ACATCCCCACCTCTTCTCTTGGTAGAGGCGGCCCGAAAGTCTAGACTCCCAAAT
GGCTCACTCAGGTCCACACCTGGACCTGGGGCACATCTCCGAGCACTCCAGTGCC
TAGCCAGGCTCCTCTGACTCCCATGCTGTAGACTGGGAGCACGGACAATGCAGGGCGC
TGGAGACCCCTGTGAGTCACACTGAGCAAGCACCCGAACACCTCTGTGCCTCAGTTT
ACTCATCTGTAAAAGGAGGAAAACAATAATTTCTTCTGCATGTGTGAATTGCAGGGC
CAGGCTCAATGACATCTTAGCAATTAGACTTTTTGAGACAGGGTCTCGCTCTGTACC
CAGGCTGGATTGAAATGGCACAATCACAGCTCACTGCAGCCTTGACCTCCAGGCTC
AAGCGATCCTCCTCCCTCAGACTCCCAAGTAGCTGAGATTACAGGCACACACCACCA
TGCCTGGTTAATTTTTGCATTTTTTGTGGACACGGGGTCTCATTATGTTGCCCAGGCT
GGTCTCCAACCTCCTGGGCTCAAACAATCCTCCTGCCTTGGCCCCCACAGTGCTGGG
ATTACAGGCATGAGCCACCATGCACGGCCACGATTATACTTACAGGTATGATTATTA
GATACATGAACATCGTTATTGTTTTCCAGCCAGGAGTCAGAGGGCAGAAAGAGCGCC
CCCCAAACCCCGGAAATCTGGGGCCTACCCAGCCTGGGTCCCAGCGCCTCCCCTCCC
TCCCTCCCTCCTGAGCTTCAGTTTCCCCAGCCCTGCTCCTGGGGTGGTAAGACCACCC
CACTAAACCCCGGGAGCCTGGGGTCCACCTAGCCCGGGTCTCAGCGCCTCCCTTCCC
TCCCTCCCTCCTCAGGCTCAGTTTCTCCAGCCCAGCTCCCAGGGTGGAAAGAGCGCC
CCCGCCAGCTCGGGAGTCTGGGGCACCCCAAGTCTGGGTCCCAGCGCCTCCTCTCCC
TAACTTCCCTCCTCAGCCTCAGTTTCCCCAGCCCTTCTCCTAGGGTAGAAAGAGCGTC
CCCCCAGCCCGGGAGTCTGGGGCCCCGCCAGCCTGGATCCCGGGGCCTCCTCTCCGT
CCCCAGCCTCAGTTTCCCCAGCCCCAGGACTCCAGGCGACCCCTCCGGCCTGCAGG
GGCAGCACGGAGCGGCCCGGGCCACCCGGAAGGGCCCCCGCCCCGCGCCGGCCCCG
CCCCGCCCCGGCTGCCCAGAACCAGGAGGCGGCGGCGGCGGGGCGGGGCCCCG
GGGCGGCGGCGGCGGGACGCGAGGACCATGGCTGCCTCCGAGCGCGCGCCTTCGC
GCACAAGATCAACAGG

FIG. 6

```

hCLASP4 -----MFPMEDISISVIGRQRTVQ----- 20
hCLASP5 -----MTHLNSLDVQLAQELG----- 16
hCLASP3 -----MAERRAFAQKISRTVAAEVRKQISGOYSGSPQLLKNLNIVG 41
hCLASP2 -----MLLFPYDDFQTAILRRQGRYICS----- 23
hCLASP7 -----MAASERRAFAHKINRTVAAEVRKQVSRERSGSPHSSRRCSSSL 43
hCLASP1 MSFRGKVFKREPSEFWKKRRTVRRV IQEEFHRFSSQEKPRLLEPLDYETVIEELEKTYRN 60
      . . .

hCLASP4 -----STVPEDA EKRAQSLFVKECIKTYSTDWHV VNYK 53
hCLASP5 -----DFT 19
hCLASP3 N-----ISHHTTVPLTEAVDPVDLEDYLITHPLAVDSGPLRDLIEFP 83
hCLASP2 -----TVPKAE EEAQSLFVTECIKTYNSDWHLVNYK 55
hCLASP7 G-----VPLTEVVEPLDFEDVLLSRPPDAEPGPLRDLVEFP 79
hCLASP1 DPLQDLLFFPSDDFSAATVSWDIRTLYSTVPEDA EHKAENLLVKEACKFYSSQWHV VNYK 120
      ::

hCLASP4 YEDFSGDFRMLPCKSLRPEKIPNHVFEIDEDCEKDED-----SSSLCSQKGGV IKG 105
hCLASP5 DDDL DVVFTPKECRTLP-SLPEEGVELDPHVR-----DCVQTYIREWLI 63
hCLASP3 PDDIEVVYSPRDCRTLVS-AVPEE-SEMDPHVR-----DCIRSYTEDWAI 126
hCLASP2 YEDYSGEFRQLPNKVVKLDKLPVHVYEVDEEVDKDED-----AASLGSQKGGITKHG 107
hCLASP7 ADDLELLLPRECRTEP-GIPKD-EKLD AQVR-----AAVEMYIEDWVI 122
hCLASP1 YEQYSGDIRQLPRAEYKPEKLP SHSFEIDHEDADKDEDTTSHSSSKGGGGAGGTGVFKSG 180
      :: . : * . : * .

hCLASP4 WLHKANVNSTIT--VTMKVFKRRYFYLTQLPDG SYILNSYKDEKNSKESK-GCIYLDACI 162
hCLASP5 VNRKNQGSPEIC--GFKKTGSRKDFHKT-LPKQTFESETLECSEPAQA--GPRHLNVLC 118
hCLASP3 VIRKYHKLGTGF--NPNTLDKQKERQKG-LPKQVFESDEAPDGNSYQDDQDDLKR SMSI 183
hCLASP2 WLYKGNMNSAIS--VTMRSFKRRFFHLIQLGDG SYNLNFYKDEKISKEPK-GSIFLDSCM 164
hCLASP7 VHRRYQYLSAAY--SPVTTDTQRERQKG-LPRQVF EQDASGDERSGPEDSND SRRGSGSP 179
hCLASP1 WLYKGNFNSTVNNTVTVR SFKKRYFQLTQLPDNSYIMNFYKDEKISKEPK-GCIFLD SCT 239
      : : . . . * : : . . .

hCLASP4 DVVQCPKMRRHAFELKMLDKYSHYLA AETE QEEME WLITLKKIIQINTDSL VQEKKETVE 222
hCLASP5 DVSGKG PVTACDFDLRSLQPDKRL ENLLQOVSAEDFEKQNEEARTN-----RQAE 169
hCLASP3 DDTPRG SWACSI FDLKNSLPDALLPNLLDRTPNEEIDRQND DQRKSN-----RHKE 234
hCLASP2 GVVQNNK VRRFAFELKMQDKSSYLLAADSEVEME EWITILNKILQLN-----FEAMQEK 219
hCLASP7 EDTPRSSGASSIFDLRNLAADSL LPSLLERAAPEDVDRRNETLRRQH-----RPPA 230
hCLASP1 GVVQNNRLRKYAFELKMNDLTYFVLA AETESDMDEWIHTLNRILQISPEGPLQGRSTEL 299
      * : : . : :

hCLASP4 TAQDD ETSS----QGAENIMASLERSMHP ELMKYGRETEQLNKL SRGDGRQNLFSFDSE 278
hCLASP5 LFALYPSVD----EEDAVEIRPVPEC PKEHLG-----N-----RILVKLLTLKFEIE 212
hCLASP3 LFALHPSPD----EEEP IERLSVPDIPKEHFG-----QRLLVKCLSLKFEIE 277
hCLASP2 RNGDSHEDD----EQSKLEGSGSGLD SYLP ELAKSAREAEIK---LKSESRVKLFYLD PD 272
hCLASP7 LLTLYPAPD----EDEAVERCSRPEPPREHFG-----QRILVKCLSLKFEIE 273
hCLASP1 TDLGLDSL DNSVTCECTPEETDSS ENNLHADFAKYLTETEDTVKTTNRMERLNLFS LDPD 359
      . : : : : : : : : : : :

hCLASP4 VQRLDFS----GIEPDIKP-FEEKCNK RFLVNCHDLTFN ILGQIGDNAKG PPTNVEPFFI 333
hCLASP5 IEPLFAS----IALYDVKERKKISENFHCDLNSDQFKGFLRAHTPSVAASSQARS AVFSV 268
hCLASP3 IEPIFAS----LALYDVKEKKKISENFYFDL NSEQMKGLLRPHVPPAAITTLARSAIFSI 333
hCLASP2 AQKLDFS----SAEPEVKS-FEEKFGKR IIVKCNDSL SNLQCCVAENEEGPTTNVEPFFV 327
hCLASP7 IEPIFGI----LALYDVREKKKISENFYFDL NSDSMKGLLRAHGTHPAISTLARSAIFSV 329
hCLASP1 IDTLKLQKKDLLEPESVIKPFEEKAAKRIMI ICKALNSNLQGCVTENENDPITNIEPFFV 419
      : : . : : : : : : : : : : :

```

hCLASP4	NLALFDVKNCKISADFHVDLNPSPVREMLWGSSTQLASDGSP---	KGSSPESYIHGIAE	390
hCLASP5	TYPSSDIYLVVKIEKVLQOQD----	IGDCAEPTYVikesdg-----	GKSKE-KIEKLKL 317
hCLASP3	TYPQDVFLVIKLEKVLQOQD----	IGECAEPMIFKEADA-----	TKNKE-KLEKLKS 382
hCLASP2	TLSLFDIKYNRKISADFHVDLNHFVRQMLATTSPALMNGS-----	GQSPSVLKGILHE	381
hCLASP7	TYPSPDIFLVIKLEKVLQOQD----	ISECCEPYMVLKEVDT-----	AKNKE-KLEKLRL 378
hCLASP1	SVALYDLRDSRKISADFHVDLNHAAVRQMLLGASVALENGNIDTITPRQSEEPHIKGLPE		479
	. . *: *: . : : . . . :		
hCLASP4	SQLRYIQOGIFSVTNPHPEIFLVARIEKVLQGNITHCAEPIKNSDPVKTAQKVHRTAKQ		450
hCLASP5	QAESFCQR-----	LGKYRMPFAWAPISLSSFFNVSTLEREVDVDSVVGRSPVGERRTLA	372
hCLASP3	QADQFCQR-----	LGKYRMPFAWTAIHLNIVSSAGSLERDSTEVEISTGERKGSWSERR	437
hCLASP2	AAMQYPKQGISVTCPPHDI FLVARIEKVLQGSITHCAEPMKSSDSSKVAQKVLKNAKQ		441
hCLASP7	AAEQFCTR-----	LGRYRMPFAWTAVHLANIVSSAGQLDRDSD----	SEGERRPAWTD RR 429
hCLASP1	EWLKFPPQAVFSVSNPHSEIVLVAKIEKVLGMNIASGAEPYIKNPDSNKYAQKILKSNRQ		539
	: : : . : : . :		
hCLASP4	VCSRLGQYRMPFAWAARPIFKDTQGSLLDGRFSPLYKQDSSKLSSEDIKLLSEYKKPE		510
hCLASP5	QSRRLSERALSLEENGVS NFKTS-----	TLSSVSSFFKQEGDRLSDEDLFKFLADYKRSS	427
hCLASP3	NSSIVGRRLERTTSGDDACNLTSFR-PATLTVTNFFKQEGDRLSDEDLFKFLADMRPS		496
hCLASP2	ACQRLGQYRMPFAWAARTLFK DASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPE		501
hCLASP7	---RRGPQ--	DRASSGDDACSFSGFR-PATLTVTNFFKQEAERLSDEDLFKFLADMRPS	483
hCLASP1	FCSKLGKYRRFAWAVRSVFKDNQGNVDRDSRESPLFRQESSKISTEDLVKLVSDYRRAD		599
	. . : : * : : : * : * : : : . . .		
hCLASP4	--KTKLQIIPGQLNITVECVFVDLSNCITSSYVPLKPFE-KNCQNITVEVEEFVPEMTKY		567
hCLASP5	SLQRRVKSIPGLLRLEISTAPEIINCLTPEMLPVKPPF-ENRTRPHKEILEFP--	TREV	484
hCLASP3	SVLRRLRPITAQLKIDISPAPENPHYCLTPELLQVKLYP-DSRVRPTREILEFP--	ARDV	553
hCLASP2	K-MAKLPVILGNLDITIDNVSSDFPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKH		560
hCLASP7	SLRRLRPVTAQLKIDISPAPENPHFCLSPPELLHIKPY-PDRGRPTKEILEFP--	AREV	540
hCLASP1	R-ISKMOTIPGSLDIAVDNVPLEHPNCVTSSFIPVKPFNMMAQTEPTVEVEEFVYDSTKY		658
	: : . * : : . . . : : : * : * : *		
hCLASP4	CYPFTIYKNHLYVYPLQLKYDSQKTFAKARNIACVCFRDSDESASALKCIYGKBPAGSV		627
hCLASP5	YVPHTVYRNLLYVYPQRLNFVN--	KLASARNITIKIQFMCG-EDASNAMPVIFGKSSGPE	541
hCLASP3	YVPNTTYRNLLYIYQSLNFAN--	RQGSARNITVKVQFMYG-EDPSNAMPVIFGKSSCSE	610
hCLASP2	TOPYTIYTNHLYVYPKYLYDSQKSF AKARNIAICIEFKDSDEEDSQPLKCIYGRGGPV		620
hCLASP7	YAPHTSYRNLLYVYPHSLNFSS--	RQGSVRNLAVRVQYMTG-EDPSQALPVI FGKSSCSE	597
hCLASP1	CRPYRVYKNQIYIYPKHLKYDSQKCFNKARNITVCIEFKNSDEESAKPLKCIYGKPEGPL		718
	* * * : : * : : . . * : : : : : . * : : : * : : .		
hCLASP4	FTTNAYAVVSHHNQNPFEYDEIKIELPIHLHQKHLLFTFYHVSCBINTKGTTKKQDTVE		687
hCLASP5	FLQBVYTA VTYHNKSPDFYEEVKIKLPKLT VNHLLFTFYHISCOQ-----	KQASVE	595
hCLASP3	FSKRAYTAVVYHNRS PDFHEEIKVKLPATLTDHHLFTFYHVSCQ-----	KONTLE	664
hCLASP2	FTRS AFAAVLHHHQNPEFYDEIKIELPTQLHEKHLLLTFFHVSCDNSSKGSTKKRDVVE		680
hCLASP7	FTRBAFTPVVYHNKSPFEYEEFKLHLPACVTENHLLFTFYHVSCQ-----	RPGTAL	651
hCLASP1	FTSAAYTAVLHHSQNPDFSDEVKIELPTQLHEKHILFSFYHVTCDINAKANAKKKEALE		778
	* . : : * : * : : * : * : : : : : : : : : : : : : : : : : *		
hCLASP4	TPVGFAWVPLLKDGRIITFEQQLPVSANLPPGYLNLNDAESRRQCNVDIKWVDGAKPLLK		747
hCLASP5	TLLGYSWLPILLNERLQTGSYCLPVALEKLPPNYSMHS AEKVPLQNPFIKWAEHGKGVFN		655
hCLASP3	TPVGYTWIPMLQNGRLKTGQFCLPVSLKPPQAYSVLSPEVP---	LPGMKWVDNHKGVFN	721
hCLASP2	TQVGYSWLPPLLKDG RVVTSEQHIPVSANLPSGHLGYQELGMGRHYGPEIKWVDGGKPLLK		740
hCLASP7	TPVGFTWIPLLQHGRRLRTGPFCLPVSDQPPPSYSVLT PDVA---	LPGMRWVDGHKGVFS	708
hCLASP1	TSVGYAWLPMLKHDQIASQEYNIPIATSLPPNYLSFQDSASGKHGGS DIKWVDGGKPLFK		838
	* : : : : : : . : *		

hCLASP4	FKSHLESTIYTQDLHVHKFFHHCQLIQS-----GSKEVPGELIKYKCLHAM	794
hCLASP5	IEVAVSSVHTQDNHLEKFFTLCHSLESQVTFPIRVLDQKISEMALEHELKLSIICLNSS	715
hCLASP3	VEVAVSSIHTQDPYLDKFFALVNALDEH-LFPVRIGDMRIMENNLLENELKSSISALNSS	780
hCLASP2	ISTHLVSTVYTQDQHLNFFQYCQKTES-----GAQALGNELVKYKSLHAM	787
hCLASP7	VELTAVSSVHPQDPYLDKFFTLVHVLEEG-AFPFRLKDTVLEGNVEQELRASLAALRLA	767
hCLASP1	VSTFVSTVNTQDPHVNAFFQECQKREKD-----MSQSPTS NFIRCKNLLNVE	887
	.. *:: ** :: * : :	:
hCLASP4	ETQVMIOFLPVLMLQLFR-----VLTNMTN-----EDDVP	824
hCLASP5	RLEPLVLFLHLVLDKLEQLSVQPMVIAGQTANFSQFAFESVVAIANSLHNSKDLSDQHG	775
hCLASP3	QLEFVVRFLHLLLDKLLLVIRPPVIAGQIVNLGQASFEAMASIIINRLHKNLEGNHDQHG	840
hCLASP2	EGHVMIAFLPTILNQLFR-----VLT-RAT-----QEEVA	816
hCLASP7	SPEPLVAFSHHVLDDKLVRLVIRPPIISGQIVNLGRGA FEAMAHVVS LVRSLAAQDARG	827
hCLASP1	KIHAIMSFLPIILNQLFK-----VLVQNE-----EDEIT	916
	. :: * : * : *	:
hCLASP4	INCTMV-LLHIVSKCHEEGLDS-----YLRSFIKYS-----FRPEKP	860
hCLASP5	RNCLLASVYHYVFRLEPVQRDPKSGAPTALLDPRS YHTYGR TSAAAVSSKLLQARVMSS	835
hCLASP3	RNSLLASYIHYVFRLPNTYPNSSSPG-PGGLGGSVHYATMARS AVR PASLNLNRSRSLSN	899
hCLASP2	VNVTRV-I IHVVAQCHEEGLES-----HLRSYVKYA-----YKAEPY	852
hCLASP7	HCPQLAAYVHYAFRLPGTEPSLPDGAPP---VTVQAATLARGSGRPASLYLARSKSISS	883
hCLASP1	TTVTRV-LPDIVAKCHEEQLDH-----SVQSYIKFV-----FKTRAC	952
	. . . :	:
hCLASP4	SAPQAQLIH-----ETLATTMIAILKQS-----	883
hCLASP5	SNPDLAGTHSAADEEVKNIMSSKIADRNC SRMSYYCSGSSDAPSSPA-----	882
hCLASP3	SNFDISGTPTSPDDEVRSIIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAESTQAMDRSC	959
hCLASP2	VASEYKTVH-----EELTKSMTTILKPS-----	875
hCLASP7	SNPD LAVAPGSVDDEVSRILASKLLHEELA-LQ-----	915
hCLASP1	KE---RPVH-----EDLAKNVTGLLKS N-----	972
	:	:
hCLASP4	-----ADFLSINKLLKYS-----WFFFEIIAKSM	907
hCLASP5	-----APRPASKKH FHEELALQ-----MNVSTGMVKSM	910
hCLASP3	NRMSSHTETSSFLQTLTGRLP TKKLFHEELALQWVVC SGSVRESALQQAWFFFEIMVKSM	1019
hCLASP2	-----ADFLTSNKLLRYS-----WFFFDVLIKSM	899
hCLASP7	-----WVVSSSAVREAILQHA-----WFFFQLMVKSM	942
hCLASP1	-----DSPTVKHVLKHS-----WFFFAILKSM	995
	. * : ***	:
Cadherin Cleavage		
hCLASP4	ATYLLLEENKIKLH RGQRF PETYHHVLHSLLLAIIPHVTIRYAEIPDE---SRNVNYSLAS	964
hCLASP5	AQHVMNDKRDSEHRTRESDRFMDITTIVNVVTSEIAALLVKPQKENEQA EKMNISLAF	970
hCLASP3	VHHLYFNDKLEAHRKSRFPERFMD DIAALVSTIASDIVSRFQKDTM---VERLNTSLAF	1076
hCLASP2	AQH LIENSKVKLI RNQRF PASYHHAETVVNMLMPHITQKFGDNPEA---SKNANHSLAV	956
hCLASP7	ALHLLLGQRLDTHRKLRFPGRF LDDITALVGSVGLVITRVHKDVEL---AEHLNASLAF	999
hCLASP1	AQH LIDTNKIQLHRPQRF PESYQNELDNLMVLS DHVWKYKDALEE---TRRATHSVAR	1052
	. :: . : * * . : : : : . . . * :	:
hCLASP4	FLKRCLTLMDRGFIFNLINDYISGFSPKDP-----KVLAEYKFEFLQTCNHEHYIPLNL	1019
hCLASP5	FLYDLSLMDRGFVENLIRHYCSQLSAKLSNL---PTLISMRLFLRILCSHEHYLNLNL	1027
hCLASP3	FLNDLLSVMDRGFVESLIKSCYQVSSKLYSLPNPSVLVSLRLDFLRIICSHEHYVTNL	1136
hCLASP2	FIKRCFTFMDRGFVEKQINNYISCFAPGDP-----KTLFEYKFEFLRVVCNHEHYIPLNL	1011
hCLASP7	FLSDLLSLVDRGFVESLVR AHYQVATRLQSSPNPAALLTLRMEFTRILCSHEHYVTNL	1059
hCLASP1	FLKRCFTFMDRGCFEKMVN NYISMFS S GDL-----KTL CQYKFD FLQEV CQHEHFIPLCL	1107
	*: : : : * * . : * : : * : * : * : * : *	:

FIG. 7
3 of 6

Cadherin EC motif

hCLASP4 PMAFAKPKLQR-----VQDS--NLEYSLSDEYCKHHFLVGLLRETSI 1060
hCLASP5 FFMNADTAPTSP--CPSISSQNSSSCSSSQDQKIASMFDLTSEYRQQHFLTGLLFTELAA 1085
hCLASP3 PCSLLTPPASPPSPSVSSATSQSSGFSTNVQDQKIANMFELSVFPQQHYLAGIVLTELAV 1196
hCLASP2 PMPFGKGRIQR-----YQDL--QLDYSLTDEFCRNHFLVGLLREVT 1052
hCLASP7 PCCPLSPPASPPSPSVSSTTSQSSTFSSQAPDPKVTSMFELSGPFRQQHFLAGILLTELAL 1119
hCLASP1 PIRSANIPDPLTP-----SES----TQELHASDMPEYSVTNEFCRKHFLIGILLREVG 1157
.

hCLASP4 ALQDN---YETRYTAISVIKNLLIKHAFDTRYQHKNQQAIAQLYLPFVGLLLENIORL 1116
hCLASP5 ALDAEGEGISKVORKAVSAIHSLLSSHDLDPRCVKPEVKVIAALYLPVGIILDALP-- 1143
hCLASP3 ILDPDAEGLFGLHKKVINMVHNLLSSHSDPRYSDPQIKARVAMLYLPLIGIIMETVP-- 1254
hCLASP2 ALQEFR---EVRLIAISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVORI 1108
hCLASP7 ALEPEAEGAFILHKKAISAVHSLLCGHDTDPRYAEATVKARVAELYPLLSIARDTLP-- 1177
hCLASP1 ALQEDQ---DVRHLALAVLKNLMKHSFDDRYREPRKQQAQIASLYMPLYGMLLDNMPRI 1213
* : : : : * * * : : * * * : : *

hCLASP4 AGRDTLYSCA-----AMPN-S---ASRDEFPCGFTSPANRGSLSLTDKDTAYGS 1160
hCLASP5 -----QL-----CDFTVADTRRYRTSGSD----- 1162
hCLASP3 -----QLY-----DFTETHNQRGRPICATDD-- 1276
hCLASP2 NVRDVSPFPVNAGMTVKDESIALPA-VNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTT 1167
hCLASP7 -----RLH-----DFAEGPGQRSRLASMLDSDTE 1201
hCLASP1 YLKDLYPFTVNTSNQGSRDDLSNNGGFQSQTAIKHANSVDTSFSKDVLSNIAAFSSIAIS 1273
. :

hCLASP4 FQ-NGHGIKREDSRGS LIPEGATGFPDQNGTGEN-----TROSSSTRSSVSQYNRLDQYE 1213
hCLASP5 -----EEQEGAGAINQNVALAIAGNNFNLKT-----SGIVLSSLPYKQYNMLNADT 1208
hCLASP3 -----YESEGSMISQTVAMAIAGTSVPQLTR----PGSFLLTSTSGRQHTTFSAES 1324
hCLASP2 STPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSE 1227
hCLASP7 -----GEGDIAGTINPSVAMAIAGGPLAPGSR----ASISQGPPTASRAGCALSAS 1249
hCLASP1 -----TVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPLALIGSTLRFDRLDQAE 1327
. : . : . : . :

hCLASP4 TRSLLMCYLYIVKMISED TLLTYWNKVSPQELINILILLEVCLFHFYRMGKRNIARVHDA 1273
hCLASP5 TRNLMICFLWIMKNADQSLIRKWIADLPSTQLNRILDLLFICVLCFEYKGKQSSDKVSTQ 1268
hCLASP3 SRSLLICLLWVLKNADET V LQKWFTDLSVLQLNRLDLLYLCVSCFEYKGKVFERNLSL 1384
hCLASP2 IKSLLMCFLYILKSMSDDALFTYWNKASTSELMDFFTISEVCLHQFYMGKRYIARNQEG 1287
hCLASP7 SRTLLACVLWVLKNTEPALLQRWATDLTLPQLGRLLDLLYLCLAAFEYKGKKAFAERINSL 1309
hCLASP1 TRSLLMCFLHIMKTISYETLIAYWQRAPSPESVDFFSILDVCLQNFYLGKRNIIRKIAA 1387
: : * * : * . : : . : : : : * * * : :

hCLASP4 WLSKHFGIDR-----KSQTMPALNRNSGVMQARLQHLSSLESS----- 1311
hCLASP5 VLQKSRDVKAR-----LEEALLRGEGARGEMRRRAPGNDRFPGLNEN--- 1311
hCLASP3 TFKKSKDMRAK-----LEEAILGSIGARQEMVRRSRGQLERSPSGSAFGSQ 1430
hCLASP2 LGPIVHDRKS-----QTLPVSRNRTGMMHARLQQLGSLDNS----- 1323
hCLASP7 TFKKSLDMKAR-----LEEAILGTIGARQEMVRRSRERSPFGNPEN----- 1350
hCLASP1 AFKFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHKQHRSTLPIIRGKN----- 1442
. : : :

hCLASP4 -----FTLNHSSTTTEADIFHQALLEGNTATEVSLTVLDTISFFITQCFKTQLL 1359
hCLASP5 --LRWKKEQTHWRQANEKLDKTKAE L DQ EALISGNLATEAHLIILDMQENIIQASS-ALD 1368
hCLASP3 ENLRWRKDMTHWRQNTTEKLDKSRAEIEHEALIDGNLATEANLIILDTLEIVQTVS-VTE 1489
hCLASP2 -----LTFNHSYGHSDADV L HQS LLEANIATEVCLTALDTLSLFTLAFKNQLL 1371
hCLASP7 --VRWRKSVTHWKQTS DRVDKTKDEMEHEALVEGNLATEASLVVLDTLEIIIVQTVM-LSE 1407
hCLASP1 --ALSNPKLLQMLDNTMTS NSNEI DIVHHVDTEANIATEGCLTILDVLSLFTQTHQRQLQ 1500
. . : : . * * * * * . .

FIG. 7
4 of 6

hCLASP4 NNDGHNPLMKKVFVDIHLAFLKNGQSEVSLKHVFASLRAFISKFPSAFFKGRVNMCAAFY 1419
hCLASP5 CKDS---LLGGVLRVLVNSLNCQSTTYLTHCFATLRALIAKFGDLLFEEVEQCDFDLCH 1425
hCLASP3 SKES---ILGGVLKVLHSMACNSAVYLQHC FATQRALVSKFPELLFEEETEQCADLCL 1546
hCLASP2 ADHGHNPLMKKVFVDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRAMCAALCY 1431
hCLASP7 ARES---VLGAVLKVVLYSLGSAQSALFLQHGLATQRALVSKFPELLFEEDTEL CADLCL 1464
hCLASP1 QCDCQNSLMKRGFDTYMLFFQVQNQSATA LKHVFASLRLFVCKFPSAFFQGPADLCGSFCY 1560
. : : : : * * * : : : * : : : * : *

hCLASP4 EVLKCCTSKISSRNEASALLYLLMRNFEYTKRKTFLRTHLQII IAVSQLIADVALSGG 1479
hCLASP5 QVLHHCSSSMDVTRSQACATLYLLMR--FSFGATSNFARVKMQVTMSLASLVGRAPDFNE 1483
hCLASP3 RLLRHCS SIGTIRSHPSASLYLLMR--QNFEIGNNFARVKMQVPMSLSSLVGTSONFNE 1604
hCLASP2 EILKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTHLQVII SVSQLIADVVGIGE 1491
hCLASP7 RLLRHCGSRISTIRTHASASLYLLMR--QNFEIGHNFARVKMQVTMSLSSLVGTTONFSE 1522
hCLASP1 EVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSHLQLIKAVSQLIADAG-IGG 1619
.: * : : : * : : : * : : : : *

hCLASP4 SRFQESLFI INNFANS DRPMKATAFPAEVKDLTKRIRTVLMATAQMKEHEKDP EMLIDLQ 1539
hCLASP5 EHLRRSLRTILAYSEEDTAMQMTFPPTQVEELL CNLNSILYDTVKMREFQEDPEMLMDLM 1543
hCLASP3 EFLRRSLKTI LTYAEEDLELRETTFPDQVQDLVFNLMILSDTVKMKEHQEDPEMLIDLQ 1664
hCLASP2 TRFQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHENDPEMLVDLQ 1551
hCLASP7 EHLRRSLKTI LTYAEEDMGLRSTFAEQVDLMFNLMILTDTVKMKEHQEDPEMLIDLQ 1582
hCLASP1 SRFQHS LAITN NFANGDKQMKNSNFP AEVKDLTKRIRTVLMATAQMKEHEKDP EMLVDLQ 1679
: : * : : : * : : : * : : : : *

transmembrane
hCLASP4 YSLAKSYASTPELRKTWLD SMAKIHVKNGD LSEAAMCYVHVAALVAEYI HRKK----- 1592
hCLASP5 YRIAKSYQASPDRLRTWLQNM AEKHTKKKCYTEAAMCLVHAAALVAEYI SMLEDH----- 1598
hCLASP3 YRIAKGYQTSPE-RLTWLQNMAGKHSERSN HAEAAQCLVHSAALVAEYI SMLEDR----- 1718
hCLASP2 YSLAKSYASTPELRKTWLD SMARIHVKNGL LSEAAMCYVHVTALVAEYI TRKG----- 1604
hCLASP7 YRIARGYQGS PDRLRTWLQNMAGKHAELGN HAEAAQCMVHAAALVAEYI ALLEDQ----- 1637
hCLASP1 YSLANSYASTPELRRTWLESMAKIHARNGD LSEAAMCYIHIAALIAEYI KRKG YWKVEKI 1739
* : : * : : * : : * : : * : : *

hCLASP4 -----LFPNGCSAFKKITPNIDE EGAMKEDAGMMD----- 1622
hCLASP5 -----SYLPVGSVSFQNISSNVLEESVVS EDTLSPDEGVD 1633
hCLASP3 -----KYLPGCVTFQNISSNVLEESAVSDDVVS PDEEGI 1753
hCLASP2 -----VFRQGCTAFRVITPNIDE EASMMEDVGMQD----- 1634
hCLASP7 -----RHLPGCVSFQNISSNVLEESAISDDILSPDEEGF 1672
hCLASP1 CTASLLSEDT HPCDSNSLLTTPSGGSMFSGWPAFLSITPNIKEGA AKEDSGMHD----- 1795
: * : * : : * : : *

ITAM
hCLASP4 ---VHYSEEVLLELLEQCVDGLWKAERYEI ISEISKLIVPIYEKRRFEKLTQVYRTLHG 1679
hCLASP5 CAGQYFTESGLVGLLEQA AELFSTGGLYETVNEVYKLVIPILEAHREFRKLTLTHSKLQR 1693
hCLASP3 CSGKYFTESGLVGLLEQA AASFMSAGMYEAVNEVYKVLIP IHEANRDAKKLSTIHGKIQE 1813
hCLASP2 ---VHFNE DVLME LLEQCADGLWKAERYELIADIYKLIPIYEKRR----- 1677
hCLASP7 CSGKHFTELGLVGLLEQAAGYFTMGGLYEAVNEVYKNLIP ILEAHRDYKKLA AVHGKIQE 1732
hCLASP1 ---TPYENILVEQLYMCGEFLWKSE RYELIADV NKP IIAVF EKQDFK KLSDLYYDIHR 1852
: * : * : : * : : *

ITAM DOCK motif DOCK motif ITAM
hCLASP4 AYTKI LEVMHTKKRLLGTFFRVAHYGQS FFEEDGKEYIYKEE KLTGLSEISRLRVKIYG 1739
hCLASP5 AFDSIVNKDH--KRMFGTYFRVGFFG-SKFGDLDEQE FVYKEEAITKLPEISHRLEAFYG 1750
hCLASP3 AFSKIVHQSTGWERMFGTYFRVGFFG-TKFGDLDEQE FVYKEEAITKLAEISHRLEGFYG 1872
hCLASP2 -----DFFEDEDGKEYIYKEE KLTPLSEISORLLKIYS 1710
hCLASP7 AFTKIMHQSSGWERVFGTYFRVGFFG-AHFGDLDEQE FVYKEESITKLAEISHRLEEFTY 1791
hCLASP1 SYLKVAEVVNSEKRLFGRYRVAHYGQGFEEEGKEYIYKEE KLTGLSEISORLLKIYA 1912
* : : : : * : : *

FIG. 7
5 of 6

	ITAM	ITAM	
hCLASP4	EKFGTENVKIIQSDSKVNAKELDPK	YAHIQVTVVKHYFDDKELTERKTEFERNHNISRFV	1799
hCLASP5	QCFGAEFVEVIKIDSTPVDKTKLDPNKAYIQI	TFVEHYFDEYEMKDRVITYFEKNFNLRRFM	1810
hCLASP3	ERFGEDVVEVIKIDSNPVDKCKLDPNKAYIQI	TYVEHYFDYEMKDRITYFDKNYNLRRFM	1932
hCLASP2	DKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVI	FFDEKELQERKTEFERSHNIRRFM	1770
hCLASP7	ERFGDDVVEIIKDSYPVDKSKLDSQKAYIQI	TYVEHYFDYELKDRVITYFDRNYGLRTFL	1851
hCLASP1	DKFGADNVKIIQDSNKNPNKDLDPKAYIQVTVTH	FFEEKEIEDRKTD FEMHHNINRFV	1972
	: ** : *::** * : .*** : *::** : * : * : * : * : * : *		
		ITAM	DOCK motif
hCLASP4	FEAPYTLGKKGQCIIEEQCKRRTILTTSNSFFYVKKRIPINCEQQIN	LKPIDGATDEIKD	1859
hCLASP5	YTPFTLEGRPRGELHEQYRRNTVLTTMHAFYIKTRISVIQKEEFV	LTPIEVAIEDMKK	1870
hCLASP3	YCTPFTLDGRAHGEHQFKRKTILTTSNAFFYIKTRVNVTHKEEII	LTPIEVAIEDMQK	1992
hCLASP2	FEMPFTQTGKRQGGVEEQCKRRTILTAIHCFYVKKRIPVMYQHHTD	LNPIEVAIDEMSK	1830
hCLASP7	FCTPFTPDGRAHGEHQHKKRKTLLSTDHAFYIKTRIRVCHREETV	LTPVEVAIEDMQK	1911
hCLASP1	FETPFTLSGKKHGGVAEQCKRRTILTTSHLFFYVKKRIQVISQSST	LNPIEVAIDEMSR	2032
	: * : * : * : * : * : * : * : * : * : * : * : *		
	Coiled-coil		
hCLASP4	KTAELOKLCSSSTDVMIQLQLKLQGVWSVQVNAGPLAYARAF	LND SQASKYPPKKVSELK	1919
hCLASP5	KTLQLAVAINQEPDAKMLQMVLCQSVGATVNQGP	LEVAQVFLAEIPADPKLYRHHNKLK	1930
hCLASP3	KTQELAFATHQDPADPKMLQMVLCQSVGTTVNQGP	LEVAQVFLSEIPSDPKLFRHHNKLK	2052
hCLASP2	KVAELRQLC SSAEVDMIKLQLKLQGVSVSVQVNAGPLAYARAF	LDDTNTKRYPDNKVKLLK	1890
hCLASP7	KTRELAFATEQDPPDAKMLQMVLCQSVGPTVNQGP	LEVAQVFLAEIPEDPKLFRHHNKLK	1971
hCLASP1	KVSELNQLCTMEEVDMISLQLKLQGVSVSVKVNAGPMAYARAF	LEETNAKKYPDNQVKLLK	2092
	* . : * * * : * . * * * : * : * : * . : . *		
	Coiled-coil		
hCLASP4	DMFRKFIAQCSIALELNERLIKEDQVEYHEGLKSNFRDMVKELSDI	IHEQILQEDTMHSP	1979
hCLASP5	LCFKEFIMRCGEAVEKNKRLITADOREYQOELKKNYNKLKENLRPM	IERKIPELYKPIFR	1990
hCLASP3	LCFKDFTKRCEPALRKNSLIGPVQKEYQRELGLSSP-----		2090
hCLASP2	EVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIM	HEQICPLEEKTS-	1949
hCLASP7	LCFKDFCKKCEPALRKNKALIGPDQKEYHRELERNYCRLREALQPI	LTORLPQLMAPTP-	2030
hCLASP1	EIFRQFADACGQALDVNERLIKEDQLEYQEELRSHYKDMSELSTVM	NEQITGRDDL SKR	2152
	* : * : * : * : * : *		
	PDZ ligand		
hCLASP4	WMSNTLHVFC AISGTSSDRGYGSPRYAEV--		2008
hCLASP5	VESQKRDSFHRSSFRCETQLSQGS-----		2015
hCLASP3	-----		
hCLASP2	VLPNSLHIFNAISGTPPTSTMVHGMTSSSSVV		1980
hCLASP7	--PGLRNSLNRASFRKADL-----		2047
hCLASP1	GVDQTCTRVISKATPALPTVSISSAEV--		2180

FIG. 7
6 of 6